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OM protein - protein search, using sw model

Run on: April 20, 2006, 12:09:49 ; Search time 189 Seconds
(without alignments)
281.295 Million cell updates/sec

File: US-10-083-849c-12

Perfect score: 631
Sequence: 1 MWALQEDTPPGSTVRRPPT.....ESLITTPSPRRPTARRRRL 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.21.*
1: geneeqp19808.*
2: geneeqp19808.*
3: geneeqp20008.*
4: geneeqp20018.*
5: geneeqp20028.*
6: geneeqp20038.*
7: geneeqp20038.*
8: geneeqp20048.*
9: geneeqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	628	99.5	121	5	AAU98752 Chicken a
2	627	99.4	121	5	AAU98742 Chicken a
3	627	99.4	121	7	AD52796 Human apo
4	627	99.4	121	7	ADM13007 Chicken a
5	626	99.2	121	7	ADM13011 Apoptin 1
6	624	98.9	121	2	AAR65201 VP3 prote
7	624	98.9	121	2	AAR88499 VP3 of ch
8	624	98.9	121	6	ABP56072 Chicken a
9	623	98.7	121	5	AAU98758 Chicken a
10	623	98.7	121	5	AAU98759 Chicken a
11	623	98.7	121	5	AAU98756 Chicken a
12	619	98.1	121	5	AAU98750 Chicken a
13	619	98.1	121	5	AAU98751 Chicken a
14	619	98.1	190	6	ABP56092 TAT-VP3 f
15	619	98.1	190	6	ABP56095 PRD4-VP3
16	619	98.1	190	6	ABP56096 PRD5-VP3
17	619	98.1	190	6	ABP56094 PRD3-VP3
18	619	98.1	422	6	ABP56097 TAT-GST-V
19	619	98.1	432	6	ABP56093 TAT-GST-V
20	619	98.1	786	6	ABR39984 CIAV prot
21	618	97.9	121	5	AAU98755 Chicken a
22	618	97.9	121	5	AAU98754 Chicken a
23	616	97.6	121	5	AAU98753 Chicken a
24	616	97.6	134	4	AAU98752 CAV apopt

25	616	97.6	140	4	AAU98752	AAU98752 standard; peptide; 121 AA.
26	616	97.6	522	6	AAU98752	AAU98752 standard; peptide; 121 AA.
27	614	97.3	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
28	611	96.8	132	5	AAU98752	AAU98752 standard; peptide; 121 AA.
29	611	96.8	132	5	AAU98752	AAU98752 standard; peptide; 121 AA.
30	611	96.8	132	5	AAU98752	AAU98752 standard; peptide; 121 AA.
31	610	96.7	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
32	607	96.2	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
33	602	95.4	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
34	602	95.4	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
35	601	95.2	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
36	600	95.1	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
37	599	94.9	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
38	599	94.9	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
39	599	94.9	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
40	599	94.9	121	5	AAU98752	AAU98752 standard; peptide; 121 AA.
41	599	94.9	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
42	599	94.9	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
43	599	94.9	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
44	598	94.8	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.
45	598	94.8	121	7	AAU98752	AAU98752 standard; peptide; 121 AA.

ALIGNMENTS

RESULT 1	AAU98752	AAU98752 standard; peptide; 121 AA.
ID	AAU98752	AAU98752 standard; peptide; 121 AA.
XX	AAU98752	AAU98752 standard; peptide; 121 AA.
AC	AAU98752	AAU98752 standard; peptide; 121 AA.
DT	27-AUG-2002	(first entry)
XX	27-AUG-2002	(first entry)
DE	Chicken anemia virus apoptin T108A mutant.	
XX	Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; muretin;	
KW	cytotoxic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2;	
KW	gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant;	
KW	Bcl-2-associated protein; Bcl-1; cell proliferation disorder;	
KW	alanine scanning; phosphorylation.	
XX	Chicken anemia virus.	
OS	Synthetic.	
EH	Key	Location/Qualifiers
FT	Misc-difference 108	/note= "Wild-type Thr substituted by Ala"
XX	MO200232954-A2.	
XX	25-APR-2002.	
PD	19-OCT-2001; 2001WO-NL000771.	
XX	20-OCT-2000; 2000EP-00203652.	
PF	20-OCT-2000; 2000US-0242397F.	
XX	(LEAD-) LEAD BV.	
PA	Noteborn MM, Rohn JL, Mumberg D, Donner P;	
XX	WPI; 2002-463306/49.	
DR	Novel isolated or recombinant phosphorylated Apoptin or its functional	
XX	equivalent or fragment, useful for detecting presence of cancer cells or	
PT	cancer prone cells, and for treating cancer or autoimmune disease.	
XX	Disclosure; Page; 62pp; English.	
PS	The invention relates to an isolated or recombinant phosphorylated	
XX	Apoptin (I) also known as VP3 or its functional equivalent and/or its	
CC	functional fragment. Apoptin induces apoptosis in human malignant and	
CC	functional fragment. Apoptin induces apoptosis in human malignant and	

transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a host cell comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the antibody, nucleic acid, a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer-inducing agent, for testing the in vitro treatment effect of Apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell proliferation or decreased cell death is observed, e.g. cancer, leukaemia or auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoptosis in the absence of functional p53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associated protein BAG-1. The present sequence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin protein sequence

Query Match 99.5%; Score 628; DB 5; Length 121;
Best Local Similarity 99.2%; Pred. No. 8.9e-61;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSRPLETPHCRERIRIGAGITITLSCGANNAPRLRGA 60
DB 1 MNALQEDTPPGSTVFRPPTSRPLETPHCRERIRIGAGITITLSCGANNAPRLRGA 60
QY 61 TADNSESSTGFKVNPDLRTDQPKPSPKRSKCDSEYRVSELKESLITTPASRPTARRR 120
DB 61 TADNSESSTGFKVNPDLRTDQPKPSPKRSKCDSEYRVSELKESLITTPASRPTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 2
AAU98742
ID AAU98742 standard; peptide; 121 AA.
AC AAU98742;
DT 27-AUG-2002 (first entry)
DE Chicken anemia virus synthesised apoptin protein.
DE 1X
DE 1X Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mitein;
KM cytotoxic; autoimmunity disease; immunosuppressive; VP3; tumour; Bcl-2;
KM gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant;
KM Bcl-2-associated protein; BAG-1; cell proliferation disorder.
XX Chicken anemia virus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 116 /note= "wild-type Lys substituted by Arg"
XX
XX WO200232954-A2.
XX
XX PD 25-APR-2002.

XX 19-OCT-2001; 2001WO-NL000771.
PF
XX 20-OCT-2000; 2000EP-00203652.
PR
XX 20-OCT-2000; 2000US-0242397P.
PR
XX (LEAD-) LEADD BV.
PA
XX Noteborn MEM, Rohm JL, Mumberg D, Donner P,
PI WPI; 2002-463306/49.
XX
XX
XX Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
PT
XX
XX Disclosure; Fig 1; 62pp; English.

The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a host cell comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the antibody, nucleic acid, a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer-inducing agent, for testing the in vitro treatment effect of Apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell proliferation or decreased cell death is observed, e.g. cancer, leukaemia or auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoptosis in the absence of functional p53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associated protein BAG-1. The present sequence is a synthesised apoptin containing a Lys to Arg mutation at position 116

Query Match 99.4%; Score 627; DB 5; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.1e-60;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSRPLETPHCRERIRIGAGITITLSCGANNAPRLRGA 60
DB 1 MNALQEDTPPGSTVFRPPTSRPLETPHCRERIRIGAGITITLSCGANNAPRLRGA 60
QY 61 TADNSESSTGFKVNPDLRTDQPKPSPKRSKCDSEYRVSELKESLITTPASRPTARRR 120
DB 61 TADNSESSTGFKVNPDLRTDQPKPSPKRSKCDSEYRVSELKESLITTPASRPTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 3
ADE52796
ID ADE52796 standard; peptide; 121 AA.
AC ADE52796;
XX
XX DT 29-JAN-2004 (first entry)

XX DE Human apoptin.
 XX OS human; apoptin; NLS; nuclear localisation signal;
 XX KW aberrant-specific apoptosis; cyostatic; immunosuppressive; gene therapy;
 XX KW cell proliferation; cancer; autoimmune disease.
 XX OS Homo sapiens.
 XX PN WO2003089467-A1.
 XX 30-OCT-2003.
 XX 18-MAR-2003; 2003WO-NL000195.
 XX 19-APR-2002; 2002EP-00076597.
 XX (LEAD-) LEADD BV.
 XX Noteborn MEM, Danen-Van Oorschot AAM;
 XX WPI; 2003-845522/78.
 XX PT New fragment of Apoptin that induces aberrant-specific apoptosis, useful
 XX PT in preparing a medicament for treating a disease associated with enhanced
 XX PT cell proliferation or decreased cell death, e.g., cancer or autoimmune
 XX PT disease.
 XX PS Claim 2; Fig 1; 46pp; English.
 XX CC The invention relates to a novel isolated or recombinant fragment of
 XX CC Apoptin that is capable of inducing aberrant-specific apoptosis. A
 XX CC peptide of the invention has cyostatic, and immunosuppressive activity,
 XX CC and may have a use in gene therapy. The fragment of Apoptin, nucleic
 XX CC acid, vector, gene delivery vehicle or host cell is useful in preparing a
 XX CC medicament for treating a disease where enhanced cell proliferation or
 XX CC decreased cell death is observed, e.g., cancer or autoimmune disease. The
 XX CC present sequence is used in the exemplification of the invention.
 XX SQ Sequence 121 AA;
 XX
 XX Query Match 99.4%; Score 627; DB 7; Length 121;
 XX Best Local Similarity 99.2%; Pred. No. 1.1e-60;
 XX Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 NNALQEDTTPGPGSTVFRPPTSSRLPTPHQREIRIGIAGITITLSCGCNNAAPTLRGA 60
 XX DB 1 NNALQEDTTPGPGSTVFRPPTSSRLPTPHQREIRIGIAGITITLSCGCNNAAPTLRGA 60
 XX QY 61 TADNSESSTGPKVVDLRTDQPKPKSKKSCDPESEYVSELKESLITTTAPSRPTARRR 120
 XX DB 61 TADNSESSTGPKVVDLRTDQPKPKSKKSCDPESEYVSELKESLITTTAPSRPTARRR 120
 XX QY 121 L 121
 XX DB 121 L 121
 XX
 XX RESULT 4
 XX ADML3007
 XX ID ADM13007 standard; protein; 121 AA.
 XX AC ADM13007;
 XX XX 20-MAY-2004 (first entry)
 XX XX Chicken anaemia virus (CAV) Apoptin.
 XX DE Apoptin; VP3; CAV; tumour-specific phosphorylation;
 XX KW tumour-specific kinase; endogenous substrate; identification;
 XX KW kinase inhibitor; kinase modulator; cell proliferative disorder;
 XX KW apoptotic disorder; cancer; autoimmune disease; cyostatic;
 XX KW immunosuppressive; gene therapy.

XX OS Chicken anaemia virus.
 XX XX
 XX FH Key Location/Qualifiers
 XX FT Protein 80..121
 XX FT /note="This fragment is an inhibitor of an aberrant-
 XX FT specific Apoptin kinase (tumour-specific kinase)"
 XX FT Misc-difference 106..110
 XX FT /note="These 5 residues are replaced by Ala-Ala-Ala-Ala-
 XX FT Ala in a loss-of-function mutant created in the
 XX FT invention"
 XX FT Misc-difference 107..108
 XX FT /note="These 2 residues are replaced by Ala-Ala in a
 XX FT loss-of-function mutant created in the invention"
 XX FT Modified-site 108
 XX FT /note="Thr is O-phosphorylated only in malignant or
 XX FT transformed cells."
 XX PN WO200308936-A1.
 XX PD 30-OCT-2003.
 XX 17-APR-2003; 2003WO-NL000294.
 XX 19-APR-2002; 2002EP-00076596.
 XX (LEAD-) LEADD BV.
 XX Noteborn MEM, Rohn JL;
 XX WPI; 2003-845561/78.
 XX DR Identifying a substrate of a kinase capable of phosphorylating Apoptin in
 XX PT an aberrant-specific way, useful in inducing apoptosis in tumor cells,
 XX PT comprises preparing aberrant and reference cells and incubating with an
 XX PT antibody.
 XX PS Example; Fig 1; 69pp; English.
 XX XX
 XX CC The invention relates to a method for identifying a substrate of a kinase
 XX CC capable of phosphorylating Apoptin (also known as VP3) in a manner
 XX CC characteristic of malignant and transformed cells (aberrant cells).
 XX CC Apoptin is a small protein derived from chicken anaemia virus (CAV) which
 XX CC induces apoptosis in malignant and transformed cells, but not in normal
 XX CC cells. This pattern of apoptotic activity is related to the finding that
 XX CC Apoptin is phosphorylated on Thr 108 in aberrant cells, whereas it is not
 XX CC phosphorylated at this position in normal cells, indicating that there is
 XX CC a tumour-specific kinase activity. The method of the invention aims to
 XX CC identify endogenous cellular substrates for this tumour-specific kinase
 XX CC and involves preparing lysates from aberrant and from normal reference
 XX CC cells; incubating the components of the lysates with a molecule capable
 XX CC of recognising phosphorylated Apoptin and phosphorylated substrate; and
 XX CC visualising the molecule, comparing the lysate components and identifying
 XX CC the substrate. The invention also relates to a substrate obtained using
 XX CC the above method; a method of obtaining a modulator of a kinase involved
 XX CC in aberrant-specific Apoptin phosphorylation; a protein inhibitor of an
 XX CC aberrant-specific Apoptin kinase; nucleic acids encoding the protein
 XX CC inhibitor; vectors, host cells and gene delivery vehicles comprising the
 XX CC nucleic acids; and methods of selecting and identifying a molecule which
 XX CC binds to both aberrant cell-specific Apoptin and a cellular protein that
 XX CC is phosphorylated in aberrant cells but not in normal cells. The tumour-
 XX CC specific kinase substrate identified according to the method of the
 XX CC invention is useful as a drug target. The inhibitor, nucleic acid,
 XX CC vector, gene delivery vehicle or host cell may be used to inhibit the
 XX CC activity of a tumour-specific kinase towards its endogenous substrate and
 XX CC is useful in the treatment of disease where enhanced cell proliferation
 XX CC or decreased cell death is observed, e.g., cancer or autoimmune disease.
 XX CC The tumour-specific kinase substrate identified according to the method
 XX CC of the invention is useful as a drug target for these disorders. The
 XX CC present sequence represents Apoptin. A C-terminal fragment of Apoptin
 XX CC (residues 80-121) is disclosed as an inhibitor of an aberrant-specific
 XX CC Apoptin kinase.

SQ Sequence 121 AA;
 Query Match 99.4%; Score 627; DB 7; Length 121;
 Best Local Similarity 99.2%; Pred. No. 1.1e-60;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNALEQEDTPGPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCGANNAPPTLRSA 60
 DB 1 MNALEQEDTPGPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCGANNAPPTLRSA 60
 QY 61 TADNSETGFKNVPLDRTDQPKPSKRSQDSEYRVSELSKSLITTPASRPTARRRIR 120
 DB 61 TADNSETGFKNVPLDRTDQPKPSKRSQDSEYRVSELSKSLITTPASRPTARRRIR 120
 QY 121 L 121
 DB 121 L 121
 RESULT 5
 ADM13011
 ID ADM13011 standard; protein; 121 AA.
 AC ADM13011;
 DT 20-MAY-2004 (first entry)
 XX Apoptin loss-of-function mutant, Tr[107-108]AA (TAA).
 DE Apoptin loss-of-function mutant, Tr[107-108]AA (TAA).
 XX Apoptin; VP3; CAV; tumour-specific phosphorylation;
 KM tumour-specific kinase; endogenous substrate; identification;
 KM kinase inhibitor; kinase modulator; cell proliferative disorder;
 KM apoptotic disorder; cancer; autoimmune disease; cytostatic;
 XX immunosuppressive; gene therapy; mutant; mutcin.
 OS Chicken anemia virus.
 OS Synthetic.
 XX WO2003089936-A1.
 PN 30-OCT-2003.
 PD 17-APR-2003; 2003WO-NL000294.
 PF 19-APR-2002; 2002BP-00076596.
 PR (LEAD-) LEADD BV.
 PA Noteborn MM, Rohn JL;
 PI Noteborn MM, Rohn JL;
 XX WPI; 2003-845561/78.
 DR Identifying a substrate of a kinase capable of phosphorylating Apoptin in
 PT an aberrant-specific way, useful in inducing apoptosis in tumor cells,
 PT comprises preparing aberrant and reference cells and incubating with an
 PT antibody.
 XX Example; Page; 69pp; English.
 RS The invention relates to a method for identifying a substrate of a kinase
 CC capable of phosphorylating Apoptin (also known as VP3) in a manner
 CC characteristic of malignant and transformed cells (aberrant cells).
 CC Apoptin is a small protein derived from chicken anaemia virus (CAV) which
 CC induces apoptosis in malignant and transformed cells, but not in normal
 CC cells. This pattern of apoptotic activity is related to the finding that
 CC Apoptin is phosphorylated on Thr 108 in aberrant cells, whereas it is not
 CC phosphorylated at this position in normal cells, indicating that there is
 CC a tumour-specific kinase activity. The method of the invention aims to
 CC identify endogenous cellular substrates for this tumour-specific kinase
 CC and involves preparing lysates from aberrant and from normal reference
 CC cells; incubating the components of the lysates with a molecule capable
 CC of recognising phosphorylated Apoptin and phosphorylated substrate; and
 CC visualising the molecule, comparing the lysate components and identifying

CC the substrate. The invention also relates to a substrate obtained using
 CC the above method; a method of obtaining a modulator of a kinase involved
 CC in aberrant-specific Apoptin phosphorylation; a protein inhibitor of an
 CC aberrant-specific Apoptin kinase; nucleic acids encoding the protein
 CC inhibitor; vectors, host cells and gene delivery vehicles comprising the
 CC nucleic acids; and methods of selecting and identifying a molecule which
 CC binds to both aberrant cell-specific Apoptin and a cellular protein that
 CC is phosphorylated in aberrant cells but not in normal cells. The tumour-
 CC specific kinase substrate identified according to the method of the
 CC invention is useful as a drug target. The inhibitor, nucleic acid,
 CC vector, gene delivery vehicle or host cell may be used to inhibit the
 CC activity of a tumour-specific kinase towards its endogenous substrate and
 CC is useful in the treatment of disease where enhanced cell proliferation
 CC or decreased cell death is observed, e.g., cancer or autoimmune disease.
 CC The tumour-specific kinase substrate identified according to the method
 CC of the invention is useful as a drug target for these disorders.
 CC Sequences ADM13010-ADM13011 represent loss-of-function Apoptin mutants
 CC which were used to demonstrate that the aberrant-specific Apoptin kinase
 CC is necessary for activating aberrant-specific apoptosis. Note: The
 CC present sequence is not shown in the specification, but was derived from
 CC the wild-type Apoptin sequence (ADM13007) and the information given on
 CC page 18.
 SQ Sequence 121 AA;
 Query Match 99.2%; Score 626; DB 7; Length 121;
 Best Local Similarity 99.2%; Pred. No. 1.5e-60;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNALEQEDTPGPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCGANNAPPTLRSA 60
 DB 1 MNALEQEDTPGPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCGANNAPPTLRSA 60
 QY 61 TADNSETGFKNVPLDRTDQPKPSKRSQDSEYRVSELSKSLITTPASRPTARRRIR 120
 DB 61 TADNSETGFKNVPLDRTDQPKPSKRSQDSEYRVSELSKSLITTPASRPTARRRIR 120
 QY 121 L 121
 DB 121 L 121
 RESULT 6
 AAR65201
 ID AAR65201 standard; protein; 121 AA.
 AC AAR65201;
 DT 25-MAR-2003 (revised)
 DT 19-AUG-1995 (first entry)
 XX VP3 protein.
 DE Chicken anemia virus VP1 protein; apoptosis; cancer therapy; vaccine;
 KM antitumor; antibody generation.
 XX Chicken anemia virus.
 OS Chicken anemia virus.
 PN WO9503414-A2.
 PD 02-FEB-1995.
 PF 19-JUL-1994; 94WO-NL000168.
 PR 20-JUL-1993; 93NL-00001272.
 PA (AESC-) AESCULAAP BV.
 XX Noteborn MM, Koch G;
 PI Noteborn MM, Koch G;
 XX WPI; 1995-075240/10.
 DR N-PsDB; Aa082830.
 XX

PT Chicken anaemia virus (CAV) mutant polypeptide(s) - useful as vaccines or
 CC for inducing apoptosis.
 XX
 PS Claim 1; Fig 3; 53pp; English.
 CC The sequence corresponds to a VP3 protein from chicken anaemia virus,
 CC (CAV), and may be used to induce apoptosis directly or to generate
 CC antibodies against CAV. The protein may be used as a vaccine or an
 CC antitumor agent. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 121 AA;
 SQ
 Query Match 98.9%; Score 624; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 2.4e-60;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLISLCCGANNAPPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLISLCCGANNAPPTLRSA 60
 QY 61 TADNSESTGFKNVPLRTDQPKPKSCDPSSEYVSELSKSLITTPSRPRTARRR 120
 DB 61 TADNSESTGFKNVPLRTDQPKPKSCDPSSEYVSELSKSLITTPSRPRTARRR 120
 QY 121 L 121
 DB 121 L 121
 QY 121 L 121
 DB 121 L 121
 RESULT 7
 ID AAR88499 standard; protein; 121 AA.
 XX AAR88499;
 AC
 XX 27-AUG-2003 (revised)
 DT 15-APR-1996 (first entry)
 DE VP3 of chicken infectious anaemia virus.
 XX
 KW Chicken infectious anaemia virus; vaccination; VP1; VP2; VP3; ss.
 XX
 OS Chicken anaemia virus (usa isolate CIA-1).
 XX
 PN WO9601116-A1.
 XX
 PD 18-JAN-1996.
 XX
 PF 05-JUL-1995; 95MO-US008440.
 XX
 PR 06-JUL-1994; 94US-00271094.
 PR 03-JUL-1995; 95US-00478086.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 PI Schat KA, Soine C, Lucio B, Renshaw R;
 XX
 DR WPI; 1996-087514/09.
 DR N-PSDB; AAT10913.
 XX
 PT Chicken infectious anaemia virus strain CIA-1 genome sequences, and novel
 PT VP1 sequence - useful to control chicken infectious anaemia such as by
 PT vaccination.
 XX
 PS Disclosure; Page 43-44; 59pp; English.
 CC The genome of the CIA-1 strain of chicken infectious anaemia virus
 CC encodes a VP-1 protein with at least four unique amino acid changes
 CC compared to the VP1 protein of other chicken infectious anaemia virus
 CC isolates. The new VP1 amino acid sequence exhibits a difference in
 CC pathogenic potential and cell tropism as compared to cell culture-adapted
 CC strains. New sequences (encoding VP1 (AAT10911), VP2 (AAT10912) and VP3
 CC (AAT10913)) and the corresponding polypeptides may be used in strategies

CC to control chicken infectious anaemia such as by vaccination. (Updated on
 CC 27-AUG-2003 to correct OS field.)
 XX
 PS Sequence 121 AA;
 SQ
 Query Match 98.9%; Score 624; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 2.4e-60;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLISLCCGANNAPPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLISLCCGANNAPPTLRSA 60
 QY 61 TADNSESTGFKNVPLRTDQPKPKSCDPSSEYVSELSKSLITTPSRPRTARRR 120
 DB 61 TADNSESTGFKNVPLRTDQPKPKSCDPSSEYVSELSKSLITTPSRPRTARRR 120
 QY 121 L 121
 DB 121 L 121
 QY 121 L 121
 DB 121 L 121
 RESULT 8
 ID ABP56072 standard; protein; 121 AA.
 XX ABP56072;
 AC
 XX 27-FEB-2003 (first entry)
 DT
 DE Chicken anaemia virus (CAV) VP3 protein.
 XX
 KW Cancer cell death; cancer; tumour; protein transduction domain; CAV;
 KW chicken anaemia virus; cytostatic; proliferative cell disorder;
 KW carcinogenesis; metastasis.
 XX
 OS Chicken anaemia virus.
 XX
 PN WO200285305-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US013092.
 XX
 PR 24-APR-2001; 2001US-0286099P.
 XX
 PA (UNIM) UNIV WASHINGTON.
 PI Dowdy SF, Ezhevsky SA, Wadia JS;
 XX
 DR WPI; 2003-093056/08.
 XX
 PT Novel fusion molecule useful for preventing or treating cancer, comprises
 PT a protein transduction domain and a chicken anaemia virus VP3 molecule.
 XX
 PS Disclosure; Page 22; 104pp; English.
 CC The present invention describes a fusion molecule (I) comprising at least
 CC one protein transduction domain (PTD) and at least one chicken anaemia
 CC virus (CAV) VP3 molecule. (I) has cytosolic activity and can be used for
 CC inducing cell death. (I) is useful for detecting cancerous or pre-
 CC cancerous cells in a mammal or for killing or injuring cancerous or pre-
 CC cancerous cells in a mammal. (I) is useful as a magnetic bullet to
 CC selectively kill cancer cells in vitro and in vivo, for inducing cell
 CC death, and for preventing or treating cancer and related proliferative
 CC disorders. (I) is also useful for studying mechanisms of carcinogenesis
 CC and metastases eukaryotic cells. (I) effectively transduces VP3 molecules
 CC directly into the cells. (I) attacks cancer and pre-cancerous cells while
 CC leaving normal cells relatively unharmed. Since more cells can be
 CC targeted by (I) when compared with past attempts using different VP3
 CC constructs, potential for patient relapse and side-effects are greatly
 CC reduced. The present sequence represents the CAV VP3 protein sequence
 CC which is given in the exemplification of the present invention

XX Sequence 121 AA;
 SQ Query Match 98.9%; Score 624; DB 6; Length 121;
 Best Local Similarity 98.3%; Pred. No. 2,4e-60;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSLGGCANAPRTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSLGGCANAPRTLRSA 60
 QY 61 TADNSETGFKKVPDLRTDQPKPSKRCSDPSEYRVELKESLITTAAPSRTARRIR 120
 DB 61 TADNSETGFKKVPDLRTDQPKPSKRCSDPSEYRVELKESLITTAAPSRTARRIR 120
 QY 121 L 121
 DB 121 L 121

RESULT 9
 AAU98758
 ID AAU98758 standard; peptide; 121 AA.
 AC AAU98758;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Chicken anemia virus apoptin T107A/T108A mutant.
 XX
 KW Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; murein;
 KW cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2;
 KW gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant;
 KW Bcl-2-associated protein; BAG-1; cell proliferation disorder;
 KW alanine scanning; phosphorylation.
 XX
 OS Chicken anemia virus.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 107.108
 FT /note= "Wild-type Thr-Thr substituted by Ala-Ala"
 XX
 PN MO200232954-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 19-OCT-2001; 2001MO-NL000771.
 XX
 PR 20-OCT-2000; 2000EP-00203652.
 PR 20-OCT-2000; 2000US-0242397P.
 XX
 PA (LEAD-) LEADD BV.
 XX
 PI Noteborn MEM, Rohn JL, Mumberg D, Donner P;
 DR WPI; 2002-463306/49.
 XX
 PT Novel isolated or recombinant phosphorylated Apoptin or its functional
 PT equivalent or fragment, useful for detecting presence of cancer cells or
 PT cancer prone cells, and for treating cancer or autoimmune disease.
 XX
 P5 Disclosure; Page; 629p; English.
 XX
 CC The invention relates to an isolated or recombinant phosphorylated
 CC Apoptin (I) also known as VP3 or its functional equivalent and/or its
 CC functional fragment. Apoptin induces apoptosis in human malignant and
 CC transformed cell lines but not in untransformed cells, by a p53
 CC independent mechanism. Apoptin is therefore a candidate therapeutic for
 CC selective destruction of tumour cells which are resistant to
 CC chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also
 CC included are a vector comprising a nucleic acid encoding apoptin, (or its
 CC functional equivalent and/or its functional fragment) which can be

CC phosphorylated and a nucleic acid encoding a kinase capable of
 CC phosphorylating apoptin, a gene delivery vehicle comprising the vector, a
 CC host cell comprising the vector or vehicle, an anti-apoptin antibody, a
 CC nucleic acid encoding the antibody, a vector comprising the antibody,
 CC Apoptin is useful for diagnostic purposes, for detecting the presence of
 CC cancer cells or cells that are cancer prone, for identifying a putative
 CC cancer-inducing agent, for testing the in vitro treatment effect of
 CC apoptin on tumour cells, and for identifying a tumour specific kinase.
 CC Compositions comprising the apoptins and antibodies are useful for
 CC treating an individual carrying a disease where enhanced cell
 CC proliferation or decreased cell death is observed, e.g. cancer, leukaemia
 CC or auto-immune disease. Apoptin is useful as a therapeutic compound for
 CC the selective destruction of tumour cells or hyperplasia, metaplasia and
 CC dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and
 CC induces apoptosis in the absence of functional p53 and cannot be blocked
 CC by Bcl-2, Bcr-abl or the Bcl-2-associated protein BAG-1. The present
 CC sequence is an apoptin mutant created during an alanine scanning
 CC experiment for mapping the phosphorylation sites in apoptin. Note: The
 CC present sequence is not shown in the specification but was created by the
 CC indexer using the information in figure 4 and the wild-type apoptin
 CC protein sequence
 CC
 CC
 SQ Sequence 121 AA;
 Query Match 98.7%; Score 623; DB 5; Length 121;
 Best Local Similarity 98.3%; Pred. No. 3.2e-60;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSLGGCANAPRTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSLGGCANAPRTLRSA 60
 QY 61 TADNSETGFKKVPDLRTDQPKPSKRCSDPSEYRVELKESLITTAAPSRTARRIR 120
 DB 61 TADNSETGFKKVPDLRTDQPKPSKRCSDPSEYRVELKESLITTAAPSRTARRIR 120
 QY 121 L 121
 DB 121 L 121

RESULT 10
 AAU98759
 ID AAU98759 standard; peptide; 121 AA.
 AC AAU98759;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Chicken anemia virus apoptin T106A/T108A mutant.
 XX
 KW Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; murein;
 KW cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2;
 KW gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant;
 KW Bcl-2-associated protein; BAG-1; cell proliferation disorder;
 KW alanine scanning; phosphorylation.
 XX
 OS Chicken anemia virus.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 106
 FT /note= "Wild-type Thr substituted by Ala"
 FT Misc-difference 108
 FT /note= "Wild-type Thr substituted by Ala"
 XX
 PN MO200232954-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 19-OCT-2001; 2001MO-NL000771.
 XX

PR	20-OCT-2000;	200OEPR-00203652.
PR	20-OCT-2000;	200OUCS-0242397P.
XX	(LEAD-) LEADD BV.	
PA	Noteborn MM,	Rohn JL, Munberg D, Donner P,
PI	WPI, 2002-463306/49.	
XX		
DR		
XX		
PT	Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.	
XX	Disclosure; Page: 62pp; English.	
PS		
XX	The invention relates to an isolated or recombinant phosphorylated Apoptin (1) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a host cell comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the antibody, a nucleic acid, a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for identifying a putative cancer-inducing agent, for testing the in vitro treatment effect of apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell proliferation or decreased cell death is observed, e.g. cancer, leukaemia or auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoptosis in the absence of functional p53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associated protein BAG-1. The present sequence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the CC indexer using the information in figure 4 and the wild-type apoptin CC protein sequence	
XX		
SX	Sequence 121 AA:	
QY	Query Match	98.7%; Score 623; DB 5; Length 121;
	Best Local Similarity	98.3%; Pred. No. 3.2e-60;
	Matches 119; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
Db	1 MNALQEDPPRSTVFRPPTSRLPEHPHCRRIRIGIGITTLSLCCGANNRAPTLISA	60
	1 MNALQEDPPPGSVIFRPPTSSRPLETPHCRIRIGIGITTLTSLCCGANRAPTLISA	60
QY	TADNSESGFNKVPDLRTDQPKPKSKSCDSEFYVELSKESLTTTPASRPRTARRR	120
Db	61 TADNSESGFNKVPDLRTDQPKPKSKSCDSEFYVELSKESLTTATAPSRRTAKRRR	120
QY	121 L 121	
Db	121 L 121	
RESULT 11		
ID	AAU98756 standard; peptide; 121 AA.	
AC	AAU98756;	
XX	27-AUG-2002 (first entry)	

XX	Chicken anemia virus Apoptin T109E mutant.
DE	
XX	Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mutcin;
XX	Cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2;
KW	gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant;
KW	Bcl-2-associated protein; Bcl-2; cell proliferation disorder;
KW	alanine scanning; phosphorylation.
XX	
OS	Chicken anemia virus.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 108 /note= "Wild-type Thr substituted by Glu"
XX	
PN	WO200232954-A2.
PD	
XX	25-APR-2002.
XX	
PF	19-OCT-2001; 2001WO-NL000771.
XX	
PR	20-OCT-2000; 2000EP-00203652.
PR	20-OCT-2000; 2000US-0242397P.
XX	
PA	(LEAD-) LEADD BV.
XX	
P1	Noteborn MEM, Roha JL, Mumberg D, Donner P;
DR	WPI; 2002-463306/49.
XX	
PT	Novel isolated or recombinant phosphorylated Apoptin or its functional
PT	equivalent or fragment, useful for detecting presence of cancer cells or
PT	cancer prone cells, and for treating cancer or autoimmune disease.
XX	
PS	Disclosure; Page; 62pp; English.
XX	
CC	The invention relates to an isolated or recombinant phosphorylated
CC	Apoptin (I) also known as VP3 or its functional equivalent and/or its
CC	functional fragment. Apoptin induces apoptosis in human malignant and
CC	transformed cell lines but not in untransformed cells, by a p53
CC	independent mechanism. Apoptin is therefore a candidate therapeutic for
CC	selective destruction of tumour cells which are resistant to
CC	chemotherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also
CC	included are a vector comprising a nucleic acid encoding apoptin, (or its
CC	functional equivalent and/or its functional fragment) which can be
CC	phosphorylated and a nucleic acid encoding a kinase capable of
CC	phosphorylating apoptin, a gene delivery vehicle comprising the vector, a
CC	host cell comprising the vector or vehicle, an anti-apoptin antibody, a
CC	nucleic acid encoding the antibody, a vector comprising the antibody,
CC	nucleic acid, a host cell comprising the antibody nucleic acid or vector,
CC	Apoptin is useful for diagnostic purposes, for detecting the presence of
CC	cancer cells or cells that are cancer prone, for identifying a putative
CC	cancer-inducing agent, for testing the in vitro treatment effect of
CC	apoptin on tumour cells, and for identifying a tumour specific kinase.
CC	Compositions comprising the apoptin and antibodies are useful for
CC	treating an individual carrying a disease where enhanced cell
CC	proliferation or decreased cell death is observed, e.g. cancer, leukaemia
CC	or auto-immune disease. Apoptin is useful as a therapeutic compound for
CC	the selective destruction of tumour cells or hyperplasia, metaplasia or
CC	dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and
CC	induces apoptosis in the absence of functional p53 and cannot be blocked
CC	by Bcl-2, Bcr-abl or the Bcl-2-associated protein Bax-1. The present
CC	sequence is an apoptin mutant created during an experiment for mapping
CC	the phosphorylation sites in apoptin. Note: The present sequence is not
CC	shown in the specification but was created by the inventor using the
CC	information in figure 4 and the wild-type apoptin protein sequence
XX	
XX	Sequence 121 AA;
XX	
XX	Query Match 98.7%; Score 623; DB 5; Length 121;
XX	Best Local Similarity 98.3%; Pred. No. 3.2e-60;
XX	Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

PD 31-OCT-2002.

XX 24-APR-2002; 2002WO-US013092.

XX 24-APR-2001; 2001US-0286099P.

XX (UNITW) UNIV WASHINGTON.

XX Dowdy SF, Ezhevsky SA, Wadia JS;

XX WPI; 2003-093056/08.

XX Novel fusion molecule useful for preventing or treating cancer, comprises

XX a protein transduction domain and a chicken anemia virus VP3 molecule.

XX Claim 36; Fig 5B; 104pp; English.

CC The present invention describes a fusion molecule (I) comprising at least
CC one protein transduction domain (PTD) and at least one chicken anaemia
CC virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for
CC inducing cell death. (I) is useful for detecting cancerous or pre-
CC cancerous cells in a mammal or for killing or injuring cancerous or pre-
CC cancerous cells in a mammal. (I) is useful as a magnetic bullet to
CC selectively kill cancer cells in vitro and in vivo, for inducing cell
CC death, and for preventing or treating cancer and related proliferative
CC disorders. (I) is also useful for studying mechanisms of carcinogenesis
CC and metastases eukaryotic cells. (I) effectively transduces VP3 molecules
CC directly into the cells. (I) attacks cancer and pre-cancerous cells while
CC leaving normal cells relatively unharmed. Since more cells can be
CC targeted by (I) when compared with past attempts using different VP3
CC constructs, potential for patient relapse and side-effects are greatly
CC reduced. The present sequence represents a PTD4-VP3 fusion protein from
CC the present invention
CC

SQ Sequence 190 AA:

Query Match 98.1%; Score 619; DB 6; Length 190;

Best Local Similarity 98.3%; Pred. No. 1.5e-59;

Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NALQEDTPPGSTVFPPPTSSRPLETPHCRIRIGIAGITITSLGCGANARAPTLRSAT 61
DB 71 NALQEDTPPGSTVFPPPTSSRPLETPHCRIRIGIAGITITSLGCGANARAPTLRSAT 130
QY 62 ADNSESTGFKNVFDLRTDQPKPPSKRSCDPSEYRVSELSKSLITTPASRPRTARRRRL 121
DB 131 ADNSESTGFKNVFDLRTDQPKPPSKRSCDPSEYRVSELSKSLITTPASRPRTARRRRL 190

Search completed: April 20, 2006, 12:13:06
Job time : 190 secs

GenCore version 5.1.7
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QM protein - protein search, using sw model

Run on: April 20, 2006, 12:13:24 ; Search time 39 Seconds

(without alignments)
298.519 Million cell updates/sec

Title: US-10-083-849c-12

Perfect score: 631

Sequence: 1 MNALEDPTPGSPSTVRPPT.....ESLITAPSPRRARRIRL 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	98.9	121	2	B39926
2	611	96.8	121	2	B48343
3	84	13.3	247	2	T32514
4	83	13.2	377	2	A48018
5	80.5	12.8	748	2	D84595
6	80	12.7	202	2	D70752
7	79.5	12.6	1082	2	T15269
8	78.5	12.4	475	2	D86209
9	78.5	12.4	587	2	T29324
10	77	12.2	348	2	S38148
11	76.5	12.1	182	2	T30760
12	76.5	12.1	353	2	A41558
13	76.5	12.1	417	2	S47539
14	76.5	12.1	481	2	S47091
15	76.5	12.1	587	2	T19893
16	76.5	12.1	982	2	T13653
17	76.5	12.1	1469	2	T09219
18	75.5	12.0	3570	2	T45025
19	75	11.9	667	2	T17221
20	75	11.9	1388	2	A53117
21	75	11.9	3507	2	T34513
22	74.5	11.8	939	2	S28394
23	74	11.7	491	1	S24354
24	73.5	11.6	648	2	PC4395
25	73.5	11.6	699	2	PC4374
26	73	11.6	173	2	S62349
27	73	11.6	278	2	S62349
28	73	11.6	493	2	S36488
29	73	11.6	631	2	A54659

30	72.5	11.5	416	2	S27198	homeotic protein H
31	72.5	11.5	486	2	S47891	exuperantia protei
32	72.5	11.5	913	2	S20590	exo-alpha-stalidas
33	72.5	11.5	929	2	T52517	hypothetical prote
34	72	11.4	298	2	AD3162	conserved hypochet
35	72	11.4	1232	2	S40766	hypothetical prote
36	72	11.4	1250	2	T22845	hypothetical prote
37	72	11.4	1622	2	JB0378	DNA (cytosine-5-)-
38	71.5	11.3	1046	2	T29776	hypothetical prote
39	71.5	11.3	2187	2	T30826	nascent polypepid
40	71	11.3	137	2	E72614	hypothetical prote
41	71	11.3	796	2	JC7355	peroxisome prolife
42	71	11.3	975	2	T48107	hypothetical prote
43	70.5	11.2	315	2	A56561	35K proline-rich p
44	70.5	11.2	407	2	T36204	hypothetical prote
45	70.5	11.2	924	2	A44945	104K microneme-tno

ALIGNMENTS

RESULT 1

B39926 hypothetical protein 2 - chicken anemia virus

C:Species: chicken anemia virus, CAV

C>Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #ext_change 05-Oct-2004

C/Accession: B39926

R:/Notebook, M.H.M., de Boer, G.F., van Roozelaar, D.J., Karreman, C., Kranenburg, O., \

J. Virol. 65, 3131-3139, 1991

A:/Title: Characterization of cloned chicken anemia virus DNA that contains all elements

A/Reference number: A39926; PMID:9123731; PMID:1851873

A/Accession: B39926

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-121 <NOT>

A/Cross-references: UNIPROT:Q99152; UNIPARC:UPI0000052846; GB:M55918; NID:G323250; PID

A/Note: This virus is unclassified.

C:/Superfamily: apoptin

Query Match 98.9%; Score 624; DB 2; Length 121;

Best Local Similarity 98.3%; Pred. No. 4.6e-52;

Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MNALEDPTPGSPSTVRPPTSRPLETPHCRRIRGIGITTLSCGCAAPPLRSA	60
DB	1	MNALEDPTPGSPSTVRPPTSRPLETPHCRRIRGIGITTLSCGCAAPPLRSA	60
QY	61	TADNSESSTGFKVVPDLRTDQPKPSKSCDSEYRVSEIKESLITTPASRRPTARRIR	120
DB	61	TADNSESSTGFKVVPDLRTDQPKPSKSCDSEYRVSEIKESLITTPASRRPTARRIR	120
QY	121	L 121	
DB	121	L 121	
RESULT 2			
B48343		hypothetical 13K protein - chicken anemia virus (isolate Cux-1)	
C:Species:		chicken anemia virus, CAV	
C>Date:		17-Feb-1994 #sequence_revision 16-Apr-1999 #ext_change 05-Oct-2004	
C/Accession:		B48343	
R:/nehan, B.W., Todd, D., Creelan, J.L., Earle, J.A., Heey, E.M., McNulty, M.S.			
Arch. Virol. 124, 301-319, 1992			
A:/Title: Characterization of viral DNAs from cells infected with chicken anaemia agent:			
A/Reference number: A48343; PMID:92296898; PMID:1605740			
A/Accession: B48343			
A/Molecule type: DNA			
A/Residues: 1-121 <ME>			
A/Cross-references: UNIPROT:Q99152; UNIPARC:UPI0000170E18; GB:M81223; NID:G323254; PID			
A/Note: the authors translated the codon ACA for residue 41 as Gly			
A/Note: sequence extracted from NCBI backbone (NCBIN:106168, NCBI:106170)			
C:/Superfamily: apoptin			

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Query Match          96.8%; Score 611; DB 2; Length 121;
Best Local Similarity 97.5%; Pred. No. 7.8e-51;
Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSPVFRPPTSSRPLETPHCKEIRIGAGITITSLGCGANARAPTLRSA 60.
DB 1 MNALQEDTPPGSPVFRPPTSSRPLETPHCKEIRIGAGITITSLGCGANARAPTLRSA 60
QY 61 TADNSETGSKNVPDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPRTARRIR 120
DB 61 TADNSETGSKNVPDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPRTARRIR 120
QY 121 L 121
DB 121 L 121

RESULT 3
T32514
hypothetical protein C44B12.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C/Accession: T32514
R./tin-Mollam, A.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid C44B12.
A/Reference number: 221183
A/Accession: T32514
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-247 <TIN>
A/Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PDB:AA88324.
A/Experimental source: strain Bristol N2; clone C44B12
C/Genetics:
A/Gene: CESP:C44B12.1
A/Map position: 4
A/Intons: 28/3; 82/1; 164/1; 192/1

Query Match          13.3%; Score 84; DB 2; Length 247;
Best Local Similarity 29.7%; Pred. No. 1.2;
Matches 35; Conservative 13; Mismatches 46; Indels 24; Gaps 6;

QY 2 NALQEDTPP-GPSTVFRPPTSSRPLETPHCKEIRIGAGITITSLGCGANARAPTLRSA 60
DB 109 NNOQYAPAPGSPFICRPP-----RPFERQACRN-----TAIYQSCONCCSISRRA 156
QY 61 TADNSETGSKNVPDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPRTARRIR 109
DB 157 GSSSVASRHRNSDDLRPEAVRQEAQEGRRKLKARPC--SMKRVLHLEKSVIQLIP 212

RESULT 4
A48018
mucin 7 precursor, salivary - human
N/Alternate names: mucin, MG2; mucin, MG2a-T1; mucin, MG2a-T2; mucin, MG2b-T2
C/Species: Homo sapiens (hmn)
C/Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A48018; S29115; S29116; S29114
R./Bobek, L.A.; Tsai, H.; Biesbrock, A.R.; Levine, M.J.
J. Biol. Chem. 268, 20563-20569, 1993
A/Title: Molecular cloning, sequence, and specificity of expression of the gene encoding
A/Reference number: A48018; MUID:9338636; PMID:7690757
A/Accession: A48018
A/Molecule type: mRNA
A/Residues: 1-377 <ROR>
A/Cross-references: UNIPROT:Q9UCD9; UNIPARC:UPI000003DBBB; GB:LJ3283
A/Experimental source: submandibular gland
A/Note: sequence extracted from NCBI backbone (NCBI:137719, NCBI:137720)
R./Reddy, M.S.; Bobek, L.A.; Haraszthy, G.G.; Biesbrock, A.R.; Levine, M.J.
Biochem. J. 287, 639-643, 1992
A/Title: Structural features of the low-molecular-mass human salivary mucin.
A/Reference number: S29114; MUID:93075006; PMID:1445223

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A/Accession: S29115
A/Molecule type: mRNA
A/Residues: 143-168 <RED>
A/Cross-references: UNIPARC:UPI0000073BF7
A/Accession: S29116
A/Molecule type: protein
A/Residues: 'S', '71-79', 'N', '81-86', 'XX', '89', 'X', '91', 'P' <RE2>
A/Cross-references: UNIPARC:UPI0000073BF7
A/Accession: S29114
A/Molecule type: protein
A/Residues: 143-145, 'X', '147', 'XXX', '151-152', 'X', '154-158', 'X', '160-161', 'A', '163-164', 'XX', '167-
A/Cross-references: UNIPARC:UPI0000073BF7
A/Genetics:
A/Gene: GDB:MUC7
A/Cross-references: GDB:138799; OMIM:156375
A/Map position: 4q13-q421
A/Keywords: glycoprotein
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-377/Product: mucin 7, salivary #status predicted <MAT>
F.97,128,135,146,312/Binding site: carbohydrate (asn) (covalent) #status predicted

```

```

Query Match          13.2%; Score 83; DB 2; Length 377;
Best Local Similarity 29.2%; Pred. No. 2.3;
Matches 31; Conservative 8; Mismatches 63; Indels 4; Gaps 1;

QY 9 PPGSPVFRPPTSSRPLETPHCKEIRIGAGITITSLGCGANARAPTLRSATADNSET 68
DB 216 PTPPATTPAPSSSAPETTPAPPTSPATTPALSSSAPETTPAVPTPSATTLDPSSA- 274
QY 69 GFKNVDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPRT 114
DB 275 ---SAPETTPAPPTSPATTPAPSSSAPETTPALITTPNSPPT 317

RESULT 5
D84595
PEARL1 4 protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84595
R./Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.
enes, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: D84595
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-746 <STO>
A/Cross-references: UNIPROT:Q9SKR5; UNIPARC:UPI00000ABFCF; GB:AE002093; NID:94803947; F
C/Genetics:
A/Gene: At2g20960
A/Map position: 2

Query Match          12.8%; Score 80.5; DB 2; Length 748;
Best Local Similarity 28.8%; Pred. No. 8.2;
Matches 36; Conservative 9; Mismatches 47; Indels 33; Gaps 5;

QY 7 DTPPGSPVFRPPTSSRPLETPHCKEIRIGAGITITSLGCGANARAPTLRSATADN-- 64
DB 199 DTPRPTPIHESATGRP-QTPETR-----PRTPDHRVATYDNRP 237
QY 65 ---SESTGKSNVPDLRTDQPKPKSKRSCDPSERYSELKESLIT-----TAPSPRTA 115
DB 238 RPIHESATGRPQPTETPRTP-EHRSALDTPRPTPIHESATGRAPQPTETPRTA 296
QY 116 RPRIR 120
DB 297 QRRGR 301

RESULT 6

```

D70752
 Probable 1pre protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: D70752
 R/Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: D70752
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A:Residues: 1-202 <COL>
 A/Cross-references: UNIPROT:Q11065; UNIPARC:UPI000012E883; GB:Z77137; GB:AL123456; NID:G
 A/Experimental source: strain H37RV
 C/Genetics:
 A:Gene: 1pre

Query Match 12.7%; Score 80; DB 2; Length 202;
 Best Local Similarity 27.2%; Pred. No. 2.2;
 Matches 28; Conservative 11; Mismatches 38; Indels 26; Gaps 5;

QY 10 PGSTVFRPPTSSRPLETHPCREIRIGITITLSLCCANARAPTLRSATDNSESTG 69
 DB 2 PG---WSPPCPTP-----RVGVVALVAATLTGCGSG---DSTVAKTPPAT- 43

QY 70 FKVPDLRTDQPKPSKRSKSCDPSEYVSELKESLTTAPSRP 112
 DB 44 ----PSLSTAHAPPPSS----EPSPSATAPPSNHAAPVDP 78

RESULT 7

T15269
 hypothetical protein F59E12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T15269

R/Johnson, D.

A:Description: The sequence of C. elegans cosmid F59E12.

A/Reference number: Z18318

A/Accession: T15269

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A:Residues: 1-1082 <JOH>

A/Cross-references: UNIPARC:UPI000017BA57; EMBL:AF003386; NID:g2088833; PID:g2088836; PI

A/Experimental source: strain Bristol N2; clone F59E12

C/Genetics:

A:Gene: CESP:F59E12.1

A/Map position: 2

A/Intons: 122/2; 193/2; 254/3; 306/3; 459/2; 819/3; 859/1

Query Match 12.6%; Score 79.5; DB 2; Length 1082;
 Best Local Similarity 27.1%; Pred. No. 15;
 Matches 36; Conservative 18; Mismatches 46; Indels 33; Gaps 8;

QY 9 PPGSTVFRPPTSSR-PLETHPCR-----EIRI-----GIAGITITSLCCANARA--- 54
 DB 542 PASPKAISHPSTPAKSPQKKTTPVEVKLEKEEDVTPSOSPATQTPRKRGR 601

QY 55 PTLRSATADNSE-STGFKVPDLRTDQPKPSKRSKSCDPSEYVSELKESLTTAPSRP 112
 DB 602 PRHSSASKTKETKPTRASPD---PLPPPSKRSKRSKESQ-----EPSTVTSKRP 651

QY 113 RTA-----RRR 118
 DB 652 RTSTVPMITRRR 664

RESULT 8

D86209
 Protein F22G5.18 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: D86209
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: D86209
 A>Status: preliminary
 A/Molecule type: DNA
 A:Residues: 1-475 <STO>
 A/Cross-references: UNIPROT:Q9JLW7; UNIPARC:UPI000009E842; GB:AE005172; NID:9878565; I
 C/Genetics:
 A:Gene: F22G5.18
 A/Map position: 1

Query Match 12.4%; Score 78.5; DB 2; Length 475;
 Best Local Similarity 23.3%; Pred. No. 7.7;
 Matches 35; Conservative 12; Mismatches 38; Indels 65; Gaps 6;

QY 2 NALQEDTPPGPST-----VFRPPTSSRPLETHPCREIRIGIAGITI 42
 DB 61 SSNQKXTPGSLPHDNLNVPYEGTEYETPAEKLFPPT---PLQTP----- 103

QY 43 TSLCCANARAPTLRSATDNSESTGFKVPDLRTDQPK 89
 DB 104 -----LPTPLPGTADNS---SMVNIIPGSSDYPPTGNGVNIIDVKARPPSPYML 149

QY 90 CDPSEY--RVSELKESLTTAPSRPTARR 117
 DB 150 CSRTAVIGLQKRLSTLQPPSPWTPNR 179

RESULT 9

T29324

hypothetical protein M01E11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004

C/Accession: T29324

R/Pauley, A.; Gattling, S.

A:Description: The sequence of C. elegans cosmid M01E11.

A/Reference number: Z20605

A/Accession: T29324

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A:Residues: 1587 <PAU>

A/Cross-references: UNIPROT:P91400; UNIPARC:UPI0000809D5; EMBL:U80450; PIDN:AA837830;

A/Experimental source: strain Bristol N2; clone M01E11

C/Genetics:

A:Gene: CESP:M01E11.6

A/Map position: 1

A/Intons: 52/1; 314/3; 460/1

Query Match 12.4%; Score 78.5; DB 2; Length 587;
 Best Local Similarity 23.3%; Pred. No. 9.7;
 Matches 24; Conservative 12; Mismatches 38; Indels 29; Gaps 1;

QY 10 PGSTVFRPPTSSRPLETHPCRIRIGITITLSLCCANARAPTLRSATDNSESTG 69
 DB 75 PERSAMAKPASCSPRI-----PTMSTASRISTLIA 105

QY 70 FKVPDLRTDQPKPSKRSKSCDPSEYVSELKESLTTAPSRP 112
 DB 113 RTA-----RRR 118
 DB 652 RTSTVPMITRRR 664

RESULT 14

S47091
cyclase-associated protein - Chlorohydra viridissima
C:Species: Chlorohydra viridissima
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47091
R:Penner, U.; Hofmann, M.; Gallio, B.; Schaller, H.C.
Submitted to the EMBL Data Library, June 1994
A:Description: The role of the cAMP pathway in mediating the effect of head activator on
A:Reference number: S47091
A:Accession: S47091
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-481 <FEN>
A:Cross-references: UNIPROT:P40122; UNIPARC:UPI0000126F0C; EMBL:X79567; NID:G498780; PID
C:Superfamily: adenyl cyclase-associated protein MCH1

Query Match 12.1%; Score 76.5; DB 2; Length 481;

Best Local Similarity 24.8%; Pred. No. 12;

Matches 31; Conservative 20; Mismatches 41; Indels 33; Gaps 7;

QY 1 MNALQEDTPPGPSTVFRPPTSSRLPETHRCREIRIGIAGITITLSLGG---CANARAPTL 57
DB 215 VSAHKPVPVPPPGCFAPPPP--PIQAP-----TTHAVTGSSESSEDSRSLF 260
QY 58 RSATADNSESSTGFKNV-----PDLRTDQPKPSKRSQPSSEYVSELKESLITTA 108
DB 261 AQLSKGSEVTAGLKVTDWKTHKNPELRN---QPPLKSSALDPPTPTPNLKK---FSA 314
QY 109 P-SRP 112
DB 315 PWSKP 319

RESULT 15

T19893

hypothetical protein C41G7.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004

C:Accession: T19893

R:Steward, C.

Submitted to the EMBL Data Library, October 1996

A:Reference number: Z19192

A:Accession: T19893

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-587 <WIL>

A:Cross-references: UNIPROT:Q93366; UNIPARC:UPI0000060F51; EMBL:Z81048; P1DN:GAB02839.1;

A:Experimental source: clone C41G7

C:Genetics:

A:Gene: CESP:C41G7.2

A:Map position: 1

A:introns: 52/1; 314/3; 460/1

Query Match 12.1%; Score 76.5; DB 2; Length 587;

Best Local Similarity 24.7%; Pred. No. 15;

Matches 36; Conservative 11; Mismatches 40; Indels 59; Gaps 6;

QY 13 STVFRPPTSSR-----PLETPHREIRIGIAGITITLSLGG-----CA 50
DB 13 STTGAPPKATRGRAAPPIKEADPATIP--KQAPG--GITIGAAACRPSPRLPGATISH 68
QY 51 NARA-----PTLSATADNSESSTGFKNVPLRTDQPKPSKRSQPS 92
DB 69 TGRASLPERSAMAKTSSGSRPALOSTSRNTTLTAASRQLRTGRPPPTGSR-----125
QY 93 SEYVSELKESLITTAASRRTARR 118
DB 126 -----TATFSLKPSVARAR 139

GenCore version 5.1.7
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QM protein - protein search, using sw model

Run on: April 20, 2006, 12:10:13 ; Search time 231 Seconds
(without alignments)
369.562 Million cell updates/sec

Title: US-10-083-849C-12

Perfect score: 631
Sequence: 1 MNALQEDTPPGSGTFRPPT.....ESLTTAPSPRTARRIRL 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	627	99.4	121	2	Q8JUV2_9CIRC
2	624	98.9	121	1	VP3_CAVCI
3	624	98.9	121	2	Q9DWX2_9CIRC
4	621	98.4	121	2	Q41448_9CIRC
5	619	98.1	121	1	VP3_CAVCI
6	619	98.1	121	2	Q9DH80_9CIRC
7	619	98.1	121	2	Q9DWX3_9CIRC
8	619	98.1	121	2	Q91N81_9CIRC
9	618	97.9	121	2	Q8JNK4_9CIRC
10	616	97.6	121	2	Q75ZFG_9CIRC
11	616	97.6	121	2	Q9DWW8_9CIRC
12	616	97.6	121	2	Q9WB33_9CIRC
13	615	97.5	121	2	Q91N45_9CIRC
14	614	97.3	121	1	VP3_CAVB2
15	614	97.3	121	2	Q9J1K0_9CIRC
16	613	97.1	121	2	Q5MAG8_9CIRC
17	612	97.0	121	2	Q39113_9CIRC
18	611	96.8	121	2	Q96F71_9CIRC
19	611	96.8	121	2	Q8JPT1_9CIRC
20	610	96.7	121	2	Q91HB6_9CIRC
21	609	96.5	121	2	Q9DWX5_9CIRC
22	608	96.4	121	2	Q9DWX6_9CIRC
23	608	96.4	121	2	Q91E24_9CIRC
24	605	95.9	121	2	Q8J032_9CIRC
25	605	95.9	121	2	Q9DWX1_9CIRC
26	604	95.7	121	2	Q91ZU6_9CIRC
27	603	95.6	121	2	Q9DWX9_9CIRC
28	591.5	93.7	120	1	VP3_CAV26
29	575	91.1	113	2	Q6R533_9CIRC
30	489	77.5	97	2	Q5XR42_9CIRC
31	489	77.5	97	2	Q5XR48_9CIRC

32	489	77.5	97	2	Q5XR51_9CIRC	Q5XR51 chicken ane
33	489	77.5	97	2	Q5XR54_9CIRC	Q5XR54 chicken ane
34	489	77.5	97	2	Q5XR57_9CIRC	Q5XR57 chicken ane
35	489	77.5	97	2	Q5XR60_9CIRC	Q5XR60 chicken ane
36	489	77.5	97	2	Q5XR63_9CIRC	Q5XR63 chicken ane
37	489	77.5	97	2	Q5XR66_9CIRC	Q5XR66 chicken ane
38	489	77.5	97	2	Q5XR69_9CIRC	Q5XR69 chicken ane
39	489	77.5	97	2	Q5XR72_9CIRC	Q5XR72 chicken ane
40	489	77.5	97	2	Q6G1G8_9CIRC	Q6G1G8 chicken ane
41	480	76.1	97	2	Q5XR45_9CIRC	Q5XR45 chicken ane
42	287	45.5	58	2	Q91N90_9CIRC	Q91N90 chicken ane
43	287	45.5	58	2	Q91N93_9CIRC	Q91N93 chicken ane
44	287	45.5	58	2	Q91N97_9CIRC	Q91N97 chicken ane
45	287	45.5	58	2	Q91N99_9CIRC	Q91N99 chicken ane

ALIGNMENTS

```

RESULT 1
ID Q8JUV2_9CIRC PRELIMINARY; PRT; 121 AA.
AC Q8JUV2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VP3 (Apoptin).
GN Name=vp3;
OS Chicken anemia virus..
OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OX NCBI_TaxId=12618;
RN RN
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14648297; DOI=10.1007/s00705-003-0189-3;
RA Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
RA Md-Zain B.M., Kono Y.;
RT "pathogenicity, sequence and phylogenetic analysis of Malaysian
RT chicken anaemia virus obtained after low and high passages in MSB-1
RT cells."
RL Arch. Virol. 148:2437-2448(2003).
RN RN
RP NUCLEOTIDE SEQUENCE.
RA Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
RA Kono Y.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN RN
RP [3]
RA NUCLEOTIDE SEQUENCE.
RA Zhong L.K., Cheng H.O., Yun L.L.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390102; AAM73651.1; -; Genomic DNA.
DR EMBL; AY171617; AAO45416.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0019051; P:induction of apoptosis by virus; IEA.
DR InterPro; IPR006958; CAV VP3.
DR Pfam; PF04771; CAV VP3; I.
SQ
SEQUENCE 121 AA; 13296 MW; D2AAB386BD61A3E CRG64;

Query Match 99.4%; Score 627; DB 2; Length 121;
Best local similarity 99.2%; Pred. No. 2.3e-50;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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VP3_SEQUENCE
VP3_CAV1
ID VP3_CAV1 STANDARD; PRT; 121 AA.
AC 099152;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apoptin (VP3).
OS Chicken anemia virus (isolate Germany Cuxhaven-1) (CAV).
OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OX NCBI_TaxID=73475;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91237831; PubMed=1851873;
RA Noreborn M.H.M., de Boer G.F., van Roozelaar D.J., Karreman C.,
RA Krennburg O., Vos J.G., Jeurissen S.H.M., Hoebe R.C., Zanema A.,
RA Koch G., van Ormondt H., van der Eb A.J.;
RT "Characterization of cloned chicken anemia virus DNA that contains all
RT elements for the infectious replication cycle.";
RL Arch. Virol. 124:301-319(1992).
CC -1- FUNCTION: May act as transcriptional regulator. Induces apoptosis
CC in infected cells. Element of infectious replication cycle.
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
CC
CC This Swiss-Prot entry is copy-right. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M55918; AAA91823.1; -; Genomic_DNA.
CC EMBL; M81223; AAA42883.1; -; Genomic_DNA.
CC DR PIR; B39926; B39926.
CC DR PIR; B48343; B48343.
CC DR InterPro; IPR006858; CAV_VP3.
CC DR Pfam; PF04771; CAV_VP3; 1.
CC KW Apoptosis; Nuclear_protein.
CC FT CONFLICT 70 70 F -> S (in Ref. 2).
CC FT CONFLICT 116 116 K -> R (in Ref. 2).
CC FT CONFLICT 118 118 R -> C (in Ref. 2).
CC SO SEQUENCE 121 AA; 13270 MW; DZAAB3869BC12A3B CRC64;
Query Match 98.9%; Score 624; DB 1; Length 121;
Best Local Similarity 98.3%; Pred. NO. 4.3e-50; Indels 0; Gaps 0;
Matches 119; Conservative 1; Mismatches 1;
OY 1 MNALEDTPPGSPVTFPRPTSSRPLETHPCHEIRIGIAGITITLSTLGCANAPAPTLRSA 60
OY 1 MNALEDTPPGSPVTFPRPTSSRPLETHPCHEIRIGIAGITITLSTLGCANAPAPTLRSA 60
DB 1 MNALEDTPPGSPVTFPRPTSSRPLETHPCHEIRIGIAGITITLSTLGCANAPAPTLRSA 60
OY 61 TADNSESTGFKNVVDLRTDQKPPSKKSCDPSSEYRVSELSKSLITTPSPRPRTARRIR 120
OY 61 TADNSESTGFKNVVDLRTDQKPPSKKSCDPSSEYRVSELSKSLITTPSPRPRTARRIR 120
DB 61 TADNSESTGFKNVVDLRTDQKPPSKKSCDPSSEYRVSELSKSLITTPSPRPRTARRIR 120
OY 121 L 121
OY 121 L 121
DB 121 L 121
RESULT 3
O9DMX2_9CIRC
ID O9DMX2_9CIRC PRELIMINARY; PRT; 121 AA.
AC O9DMX2;

```

DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE VP3 protein.
 GN Name=VP3;
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxID=12618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21296594; PubMed=11402859; DOI=10.1007/s007050170141;
 RA Scott A.N.J., McNulty M.S., Todd D.;
 RT "Characterisation of a chicken anaemia virus variant population that
 RT resists neutralisation with a group-specific monoclonal antibody."
 RL Arch. Virol. 146:713-728(2001).
 DR EMBL, AJ297682; CACI4758.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro; IPR006858; CAV VP3.
 DR Pfam; PF04771; CAV VP3; I.
 SO SEQUENCE 121 AA; 13284 MW; 82AB3865CCBACE5 CRC64;
 Query Match 98.9%; Score 624; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 4,3e-50;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
 QY .1 MNALQETPPGPGSVFRFPPTSSRPLEPHCRERFIIGAGITITSLGCGANARAPTLSA 60
 DBR 1 MNALQDTPPPSPVFRFPPTSSRPLEPHCRERFIIGAGITITSLGCGANARAPTLSA 60
 QY 61 TADNSETGFKNVPDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPTARRIR 120
 DB 61 TADNSETGFKNVPDLRTDQPKPKSKRSCDPSERYSELKESLITTPASRPTARRIR 120
 QY - 121 L 121
 DB 121 L 121
 RESULT 4
 O41448_9CIRC O41448_9CIRC PRELIMINARY; PRT; 121 AA.
 AC O41448;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Cloned isolate 10, complete genome (VP3).
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxID=12618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92296898; PubMed=1605740;
 RA Meenan B.M., Todd D., Creelan J.L., Earle J.A.P., Hoey E.M.,
 McNulty M.S.;
 RT "Characterization of viral DNAs from cells infected with chicken
 RT anaemia agent: sequence analysis of the cloned replicative form and
 RT transfection capabilities of cloned genome fragments."
 RL Arch. Virol. 124:301-319(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RT Todd D., Connor T.J., Calvert V., Creelan J.L., Meenan B.M.,
 McNulty M.S.;
 RT "Molecular cloning of an attenuated chicken anaemia virus isolate
 RT following repeated cell culture passage."
 RL Avian Pathol. 24:171-187(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98001355; PubMed=9343191;
 RA Meenan B.M., Todd D., Creelan J.L., Connor T.J., McNulty M.S.;
 RT "Investigation of the attenuation exhibited by a molecularly cloned
 RT chicken anaemia virus isolate by utilizing a chimeric virus approach";
 J. Virol. 71:8362-8367(1997).
 LT

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RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RA      McKenna G.F.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U66304; AAC58477.1; -; Genomic DNA.
DR      EMBL; AJ536295; CAD60259.1; -; Genomic DNA.
DR      GO; GO:0042025; C:induction of apoptosis by virus; IEA.
DR      GO; GO:0019051; P:induction of apoptosis by virus; IEA.
DR      InterPro; IPR006858; CAV_VP3.
DR      Pfam; PF04771; CAV_VP3; 1.
SQ      SEQUENCE 121 AA; 13312 MW; E4AAB75960F2C5C5 CRC64;

Query Match      98.4%; Score 621; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 8.2e-50;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60
DB      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60
QY      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
DB      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
QY      121 L 121
DB      121 L 121

RESULT 5
VP3_CAVCI STANDARD; PRT; 121 AA.
ID VP3_CAVCI
AC P54094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apoptin (VP3).
OS Chicken anemia virus (Isolate USA CIA-1) (CAV).
OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OC NCBI_TaxID=73478;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=897126092; PubMed=8971016;
RA      Renshaw R.W., Soine C., Weinkle T., O'Connell P.H., Ohashi K.,
RA      Watson S., Lucio B., Harrington S., Schat K.A.;
RT      "A hypervariable region in VP1 of chicken infectious anemia virus
RT      mediates rate of spread and cell tropism in tissue culture.";
RL      J. Virol. 70:8872-8878(1996).
RN      [2]
RP      SEQUENCE REVISION TO 50.
RA      Renshaw R.W.;
RL      Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: May act as transcriptional regulator. Induces apoptosis
CC      in infected cells. Element of infectious replication cycle.
CC      -1- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
DR      EMBL; L14767; AA009423.1; -; Genomic DNA.
DR      InterPro; IPR006858; CAV_VP3.
DR      Pfam; PF04771; CAV_VP3; 1.
DR      Apoptosis; Nuclear protein.
DR      Apoptosis; Nuclear protein.
SQ      SEQUENCE 121 AA; 13245 MW; D2AAB39C2BD61A3E CRC64;

Query Match      98.1%; Score 619; DB 1; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.3e-49;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60

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DB      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60
QY      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
DB      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
QY      121 L 121
DB      121 L 121

RESULT 6
Q9DHB0_9CIRC PRELIMINARY; PRT; 121 AA.
ID Q9DHB0_9CIRC
AC Q9DHB0;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
DE VP3 protein.
GN Name=VP3;
OS Chicken, anemia virus.
OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OC NCBI_TaxID=12618;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=21296594; PubMed=11402858; DOI=10.1007/s007050170141;
RA      Scott A.N.J., McNulty M.S., Todd D.;
RT      "Characterisation of a chicken anaemia virus variant population that
RT      resists neutralisation with a group-specific monoclonal antibody.";
RL      Arch. Virol. 146:713-728(2001).
DR      EMBL; AJ297683; CAC14761.1; -; Genomic DNA.
DR      EMBL; AJ297679; CAC14749.1; -; Genomic DNA.
DR      EMBL; AJ297680; CAC14752.1; -; Genomic DNA.
DR      GO; GO:0042025; C:host cell nucleus; IEA.
DR      GO; GO:0019051; P:induction of apoptosis by virus; IEA.
DR      InterPro; IPR006858; CAV_VP3.
DR      Pfam; PF04771; CAV_VP3; 1.
SQ      SEQUENCE 121 AA; 13272 MW; 33EFA7D7CA93013F CRC64;

Query Match      98.1%; Score 619; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.3e-49;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60
DB      1 MNALEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSGCGANRAPTLRSA 60
QY      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
DB      61 TADNSETGFKVVPDLRTDQPKPSKRCSDPSEYVSELKSLITTTAPSRPTARRR 120
QY      121 L 121
DB      121 L 121

RESULT 7
Q9DMX3_9CIRC PRELIMINARY; PRT; 121 AA.
ID Q9DMX3_9CIRC
AC Q9DMX3;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE VP3 protein.
GN Name=VP3;
OS Chicken anemia virus.
OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OC NCBI_TaxID=12618;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=21296594; PubMed=11402858; DOI=10.1007/s007050170141;
RA      Scott A.N.J., McNulty M.S., Todd D.;

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"Characterisation of a chicken anaemia virus variant population that resists neutralisation with a group-specific monoclonal antibody.";
 RT Arch. Virol. 146:713-728(2001).
 RL EMBL: AJ297681; CAC14755.1; -; Genomic DNA.
 DR GO: GO:0042025; C:host cell nucleus; IEA.
 DR GO: GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro: IPR006858; CAV_VP3.
 DR Pfam: PF04771; CAV_VP3; I.
 DR SEQUENCE 121 AA; 13329 MW; A47IDF69BD61A3F CRC64;
 SO
 Query Match 98.1%; Score 619; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 1.3e+49;
 Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNALEDTPPGSPVFPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTURSA 60
 DB 1 MNALEDTPPGSPVFPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTURSA 60
 QY 61 TANDSESTGKKNVPLDTDPKPKSKRSCDPSFYRSEKESLITAPSPRTARRRIR 120
 DB 61 TANDSESTGKKNVPLDTDPKPKSKRSCDPSFYRSEKESLITAPSPRTARRRIR 120
 QY 121 L 121
 DB 121 L 121
 RESULT 8
 ID 091NB1_9CIRC PRELIMINARY; PRT; 121 AA.
 AC 091NB1_9CIRC
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE VP3.
 GN Name=VP3;
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxID=12618;
 RX MEDLINE=21310375; PubMed=11417817;
 RT "Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama."
 RL Avian Dis. 45:373-388(2001).
 RP NUCLEOTIDE SEQUENCE.
 RA van Santen V.L., Toro H., Hoerr F.J.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=AA2;
 RA Yamaguchi S., Kaji N., Munangandu H.M., Kojima C., Mase M.,
 RA Tsukamoto K.;
 RT "Quantitation of chicken anemia virus by competitive polymerase chain reaction."
 RL Avian Pathol. 29:305-310(2000).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21195622; PubMed=11287698;
 RA Yamaguchi S., Imada T., Kaji N., Mase M., Tsukamoto K., Tanimura N.,
 RT "Identification of a genetic determinant of pathogenicity in chicken anaemia virus."
 RL J. Gen. Virol. 82:1233-1238(2001).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Delrose;
 RA Wu Z.Q., Li G.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [6]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14648297; DOI=10.1007/s00705-003-0189-3;
 RA Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
 RA Mo-Zain B.M., Kono Y.;
 RT "Pathogenicity, sequence and phylogenetic analysis of Malaysian RT chicken anaemia virus obtained after low and high passages in MSB-1 cells."
 RL Arch. Virol. 148:2437-2448(2003).
 RP NUCLEOTIDE SEQUENCE.
 RA Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
 RA Kono Y., Datus A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA Spackman E., Rosenberger J.K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA Spackman E., Rosenberger J.K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
 Kono Y.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA He C.Q., Li Y.L.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Namakkal-Indian;
 RA Jadhao S.J., Pattnaik B., Toshniwal R.M., Dash B.B., Pradhan H.K.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=LP4;
 RA Liang Z.;
 RT "Cloning and sequencing of chicken anemia virus isolate LP4."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=TJBD33;
 RA Liang Z.;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=SD24;
 RA Liang Z.X.;
 RT "Chicken anemia virus."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF311900; AAK70849.2; -; Genomic DNA.
 DR EMBL: AB031296; BAA90490.1; -; Genomic DNA.
 DR EMBL: AB046587; BAB19636.1; -; Genomic DNA.
 DR EMBL: AB046588; BAB19639.1; -; Genomic DNA.
 DR EMBL: AB046589; BAB19642.1; -; Genomic DNA.
 DR EMBL: AB046590; BAB19645.1; -; Genomic DNA.
 DR EMBL: AF199501; AAF08299.1; -; Genomic DNA.
 DR EMBL: AF285882; AAK83007.1; -; Genomic DNA.
 DR EMBL: AF313470; AAG34178.1; -; Genomic DNA.
 DR EMBL: AF372658; AAK54239.1; -; Genomic DNA.
 DR EMBL: AF390038; AAL98996.1; -; Genomic DNA.
 DR EMBL: AF475508; AAL79914.1; -; Genomic DNA.
 DR EMBL: AF520788; AAM75347.1; -; Genomic DNA.
 DR EMBL: AY839944; AAM02946.1; -; Genomic DNA.
 DR EMBL: AY843527; AAM30191.1; -; Genomic DNA.
 DR EMBL: AY999018; AAY15241.1; -; Genomic DNA.
 DR GO: GO:0042025; C:host cell nucleus; IEA.
 DR GO: GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro: IPR006858; CAV_VP3.
 DR Pfam: PF04771; CAV_VP3; I.
 SO SEQUENCE 121 AA; 13245 MW; D2AAB39C2BD61A3E CRC64;
 [6]

Query Match 98.1%; Score 619; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 1.3e-49;
 Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60

QY 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120
 DB 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120

QY 121 L 121
 DB 121 L 121

RESULT 9
 Q8UNK4_9CIRC PRELIMINARY; PRT; 121 AA.
 ID Q8UNK4_9CIRC PRELIMINARY; PRT; 121 AA.
 AC Q8UNK4;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE VP3.
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxId=12618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14648297; DOI=10.1007/s00705-003-0189-3;
 RA Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
 RA Md-Zain B.M., Kono Y.;
 RT "Pathogenicity, sequence and phylogenetic analysis of Malaysian
 RT Chicken anaemia virus obtained after low and high passages in MSB-1
 RT cells.";
 RL Arch. Virol. 148:2437-2448 (2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
 RA Kono Y.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY040632; AK82947.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro; IPR006858; CAV_VP3.
 DR Pfam; PF04771; CAV_VP3; 1.
 SQ SEQUENCE 121 AA; 13338 MW; CD34CA7E9BD61A3E CRC64;

Query Match 97.9%; Score 618; DB 2; Length 121;
 Best Local Similarity 98.3%; Pred. No. 1.5e-49;
 Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60

QY 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120
 DB 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120

QY 121 L 121
 DB 121 L 121

RESULT 10
 Q75ZP9_9CIRC PRELIMINARY; PRT; 121 AA.
 ID Q75ZP9_9CIRC PRELIMINARY; PRT; 121 AA.
 AC Q75ZP9;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE VP3.
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxId=12618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=66;
 RA Imai K., Yamaguchi S.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB119448; BAD12197.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro; IPR006858; CAV_VP3.
 DR Pfam; PF04771; CAV_VP3; 1.
 SQ SEQUENCE 121 AA; 13272 MW; DA082253B28FAD0 CRC64;

Query Match 97.6%; Score 616; DB 2; Length 121;
 Best Local Similarity 97.5%; Pred. No. 2.4e-49;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60

QY 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120
 DB 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120

QY 121 L 121
 DB 121 L 121

RESULT 11
 Q9DWM8_9CIRC PRELIMINARY; PRT; 121 AA.
 ID Q9DWM8_9CIRC PRELIMINARY; PRT; 121 AA.
 AC Q9DWM8;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE VP3 protein.
 GN Name=VP3;
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 OX NCBI_TaxId=12618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21296594; PubMed=11402858; DOI=10.1007/s007050170141;
 RA Scott A.N.V., McNulty M.S., Todd D.;
 RT "Characterisation of a chicken anaemia virus variant population that
 RT resists neutralisation with a group-specific monoclonal antibody.";
 RL Arch. Virol. 146:713-726 (2001).
 DR EMBL; AJ297686; CAC14770.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro; IPR006858; CAV_VP3.
 DR Pfam; PF04771; CAV_VP3; 1.
 SQ SEQUENCE 121 AA; 13240 MW; D7ABB05D37A61A3E CRC64;

Query Match 97.6%; Score 616; DB 2; Length 121;
 Best Local Similarity 97.5%; Pred. No. 2.4e-49;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60
 DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGAGITTTLSGCGANAPAPTLRSA 60

QY 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120
 DB 61 TADNSESSTGFKVVPDLRTDQPKPKSKKSCDSEYRVSELSKSLITTTAPSRPTARRRIR 120

QY 121 L 121
 DB 121 L 121

Db 121 L 121

RESULT 12

09MB33_9CIRC PRELIMINARY; PRT; 121 AA.

AC 09MB33;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-FEB-2005 (TREMblrel. 29, Last annotation update)
 DE V33.
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 NCBI_TaxID=12618;
 RN NUCLEOTIDE SEQUENCE.

RP STRAIN=TR20;
 RA Okamura H., Sakaguchi M., Tokunaga E.;
 RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RC NUCLEOTIDE SEQUENCE.

RC STRAIN=BD-3;
 RX MEDLINE=2307954; PubMed=12420868;
 RX DOI=10.1046/j.1439-0450.2002.00581.x;
 RA Islam M.R., Johne R., Raue R., Todd D., Muller H.;
 RT "Sequence analysis of the full-length cloned DNA of a chicken anaemia virus (CAV) strain from Bangladesh: evidence for genetic grouping of CAV strains based on the deduced VP1 amino acid sequences.";
 RT J. Vet. Med. B Infect. Dis. Vet. Public Health 49:332-337(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BD-3;
 RA Islam M.R., Johne R., Raue R., Todd D., Muller H.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB027470; BAA77833.1; -; Genomic DNA.
 DR EMBL: AF395114; AA020898.1; -; Genomic DNA.
 DR GO: GO:0042025; C:host cell nucleus; IEA.
 DR GO: GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro: IPR006858; CAV VP3.
 DR Pfam: PF04771; CAV VP3; I.
 SO SEQUENCE 121 AA; 13272 MW; 72B7A9C2BD60E88 CRC64;

Query Match 97.6%; Score 616; DB 2; Length 121;
 Best Local Similarity 97.5%; Pred. No. 2.4e-49;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNAIQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTSLGCGANARAPTLRSA 60
 DB 1 MNAIQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTSLGCGANARAPTLRSA 60
 QY 61 TADNSETGKXVVDLRTDQPKPKSKSCDPSERYSELKESLITTAAPSPTARRRIR 120
 DB 61 TADNSETGKXVVDLRTDQPKPKSKSCDPSERYSELKESLITTAAPSPTARRRIR 120
 QY 121 L 121
 DB 121 L 121

RESULT 13
 091NA5_9CIRC PRELIMINARY; PRT; 121 AA.
 AC 091NA5;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE V33.
 OS Chicken anemia virus.
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 NCBI_TaxID=12618;
 RN NUCLEOTIDE SEQUENCE.

RX MEDLINE=21310375; PubMed=11417817;
 RA van Santen V.L., Li L., Hoerr F.J., Lauerman L.H.;
 RT "Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama."
 RL Avian Dis. 45:373-388(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA van Santen V.L., Toro H., Hoerr F.J.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF311892; AA070825.2; -; Genomic DNA.
 DR GO: GO:0042025; C:host cell nucleus; IEA.
 DR GO: GO:0019051; P:induction of apoptosis by virus; IEA.
 DR InterPro: IPR006858; CAV VP3.
 DR Pfam: PF04771; CAV VP3; I.
 SO SEQUENCE 121 AA; 13231 MW; B4AAB39C2DD618AC CRC64;

Query Match 97.5%; Score 615; DB 2; Length 121;
 Best Local Similarity 97.5%; Pred. No. 2.9e-49;
 Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNAIQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTSLGCGANARAPTLRSA 60
 DB 1 MNAIQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTSLGCGANARAPTLRSA 60
 QY 61 TADNSETGKXVVDLRTDQPKPKSKSCDPSERYSELKESLITTAAPSPTARRRIR 120
 DB 61 TADNSETGKXVVDLRTDQPKPKSKSCDPSERYSELKESLITTAAPSPTARRRIR 120
 QY 121 L 121
 DB 121 L 121

RESULT 14

VP3_CAV82 STANDARD; PRT; 121 AA.

AC P54096;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Apoptin (VP3).
 OS Chicken anemia virus (isolate Japan 82-2) (CAV).
 OC Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
 NCBI_TaxID=73476;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX MEDLINE=95297149; PubMed=7778281;
 RA Kato A., Fujino M., Nakamura T., Ishihama A., Otsaki Y.;
 RT "Gene organization of chicken anemia virus."
 RL Virology 209:480-488(1995).
 CC -1- FUNCTION: May act as transcriptional regulator. Induces apoptosis in infected cells. Element of infectious replication cycle.
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL: D31965; BAA06733.1; -; Genomic DNA.
 DR InterPro: IPR006858; CAV VP3.
 DR Pfam: PF04771; CAV VP3; I.
 KW Apoptosis; Nuclear protein.
 SO SEQUENCE 121 AA; 13233 MW; C770839C2BD61A3E CRC64;

Query Match 97.3%; Score 614; DB 1; Length 121;
 Best Local Similarity 97.5%; Pred. No. 3.6e-49;
 Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 DB 1 MNAIQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTSLGCGANARAPTLRSA 60

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QY      121 L 121
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DB      121 L 121

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RESULT 15

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DT      01-OCT-2000 (TEMBLrel. 15, Created)
DT      01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE      01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE      VP-3 Protein.
OS      Chicken anemia virus.
OC      Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
OX      NCBI_TaxID=12618;
RN      (1)
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=SH-1;
RX      MEDLINE=20381181; PubMed=10900046;
RA      Cardona C.J., Oswald W.B., Schat K.A.;
RT      "Distribution of chicken anaemia virus in the reproductive tissues of
RT      specific-pathogen-free chickens."
RL      J. Gen. Virol. 81:2067-2075(2000).
DR      EMBL; AF214563; AAF37220.1; -; Genomic DNA.
DR      GO; GO:0042025; C:host cell nucleus; IEA.
DR      GO; GO:0019051; P:induction of apoptosis by virus; IEA.
DR      InterPro; IPR006858; CAV_VP3.
DR      Pfam; PF04771; CAV_VP3; 1.
SQ      SEQUENCE 121 AA; 13215 MW; 22AAB38D3ACB153 CRC64;

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Query Match

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Best Local Similarity 97.3%; Score 614; DB 2; Length 121;
Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      61 TADNSETGPKVNPDLRTDQPKPKSKKSCDPSEYRVSELKESLITTPSPRTARRRIR 120
QY      121 L 121
      |
DB      121 L 121

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Search completed: April 20, 2006, 12:17:04
 Job time : 233 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using SW model

Run on: April 20, 2006, 12:17:18 ; Search time 47 Seconds
(without alignments)
212.846 Million cell updates/sec

Title: US-10-083-849c-12

Perfect score: 631
Sequence: 1 MNALEDPTPGSTVFRPPT.....ESLITTPSRPRTRRRRL 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB pep:*
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- 3: /cgn2_6/prodata/1/1aa/7 COMB pep:*
- 4: /cgn2_6/prodata/1/1aa/8 COMB pep:*
- 5: /cgn2_6/prodata/1/1aa/9 COMB pep:*
- 6: /cgn2_6/prodata/1/1aa/10 COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	98.9	121	US-08-489-666C-7	Sequence 7, Appl
2	624	98.9	121	US-08-911-092-7	Sequence 7, Appl
3	624	98.9	121	US-08-485-001B-7	Sequence 7, Appl
4	624	98.9	121	US-08-454-121A-7	Sequence 7, Appl
5	624	98.9	121	US-08-482-161B-7	Sequence 7, Appl
6	624	98.9	121	US-09-057-963A-6	Sequence 6, Appl
7	616	97.6	134	US-09-645-415A-58	Sequence 58, Appl
8	616	97.6	140	US-09-645-415A-60	Sequence 60, Appl
9	88.5	14.0	757	US-09-252-991A-25918	Sequence 25918, A
10	85	13.5	488	US-09-252-991A-30531	Sequence 30531, A
11	83.5	13.2	133	US-09-252-991A-25561	Sequence 25561, A
12	83.5	13.2	184	US-09-252-991A-24427	Sequence 24427, A
13	82	13.0	195	US-09-252-991A-26926	Sequence 26926, A
14	81.5	12.9	135	US-09-252-991A-28784	Sequence 28784, A
15	81	12.8	765	US-09-502-540-10602	Sequence 10602, A
16	79.5	12.6	285	US-09-252-991A-22267	Sequence 22267, A
17	78.5	12.4	205	US-09-270-767-59394	Sequence 59394, A
18	78.5	12.4	373	US-09-252-991A-29008	Sequence 29008, A
19	78.5	12.4	380	US-09-270-767-43987	Sequence 43987, A
20	78	12.4	222	US-09-252-991A-32998	Sequence 32998, A
21	77.5	12.3	222	US-09-252-991A-27628	Sequence 27628, A
22	77	12.2	348	US-09-315-794-42	Sequence 42, Appl
23	77	12.2	348	US-09-389-341-42	Sequence 42, Appl
24	76.5	12.1	156	US-09-252-991A-20938	Sequence 20938, A
25	76	12.0	160	US-09-270-767-41118	Sequence 41118, A
26	76	12.0	160	US-09-270-767-56334	Sequence 56334, A
27	76	12.0	162	US-08-728-323A-2	Sequence 2, Appl

28	76	12.0	1162	2	US-09-298-568-2	Sequence 2, Appl
29	76	12.0	1162	2	US-09-410-399-2	Sequence 2, Appl
30	76	12.0	1162	2	US-09-894-273-2	Sequence 2, Appl
31	75.5	12.0	1027	2	US-09-162-021B-2	Sequence 2, Appl
32	75.5	12.0	1027	2	US-10-268-051-8	Sequence 8, Appl
33	75.5	12.0	1027	2	US-10-125-772-2	Sequence 2, Appl
34	75	11.9	196	2	US-09-252-991A-23646	Sequence 23646, A
35	75	11.9	288	2	US-09-270-767-46140	Sequence 46140, A
36	75	11.9	393	2	US-09-252-991A-32055	Sequence 32055, A
37	75	11.9	1805	2	US-09-949-016-8246	Sequence 8246, Ap
38	74.5	11.8	260	2	US-09-252-991A-21611	Sequence 21611, A
39	74.5	11.8	694	2	US-08-559-397A-31	Sequence 31, Appl
40	74.5	11.8	939	2	US-08-487-558B-380	Sequence 380, App
41	74	11.7	154	2	US-09-252-991A-23167	Sequence 23167, A
42	74	11.7	491	1	US-07-903-103-2	Sequence 2, Appl
43	74	11.7	491	1	US-08-044-619A-2	Sequence 2, Appl
44	74	11.7	491	1	US-08-283-911-2	Sequence 2, Appl
45	74	11.7	491	1	US-08-245-500A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-489-666C-7
Sequence 7, Application US/08489666C
Patent No. 5922600
GENERAL INFORMATION:
APPLICANT: No. 5922600eborn, M.H.M
APPLICANT: Koch, G.
TITLE OF INVENTION: Chicken Anemia Virus mutants and
TITLE OF INVENTION: vaccines and uses based on the viral proteins VP1, VP2 and
TITLE OF INVENTION: VP3 or sequences of that virus coding therefor.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSER: RAE-VENTER LAW, P.C.
STREET: 260 SHERIDAN AVE., P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08489,666C
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
FILING DATE: 06-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 94/00168
FILING DATE: 19-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LBBV.003.04US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400

TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULAR TYPE: protein
HYPOTHEICAL: NO
US-08-489-666C-7

Query Match 98.9%; Score 624; DB 1; Length 121;
Best Local Similarity 98.3%; Pred. No. 2,4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 121 L 121
DB 121 L 121

RESULT 2
US-08-911-092-7
Sequence 7, Application US/08911092
Patent No. 5952002

GENERAL INFORMATION:
APPLICANT: No. 5952002eborn, Mathews H.M.

APPLICANT: Koch, Guus
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: And Uses Based On The Viral Proteins VP1, VP2, And VP3 Or
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSER: Rae-Venter Law Group, P.C.
STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,092
FILING DATE: 14-AUG-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOV-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-JULY-1994

APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993

APPLICATION NUMBER: US 08/030,335
FILING DATE: 8-MAR-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV003.00U51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULAR TYPE: protein
HYPOTHEICAL: NO
US-08-911-092-7

Query Match 98.9%; Score 624; DB 1; Length 121;
Best Local Similarity 98.3%; Pred. No. 2,4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITITLSLGGCANAPATLRS 60
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DB 61 TADNSETGFKNVPDLRTDQPKPSKRS CDPSERYVSELKESLITTPSPRTARRIR 120
QY 121 L 121
DB 121 L 121

RESULT 3
US-08-485-001B-7
Sequence 7, Application US/08485001B
Patent No. 5981502

GENERAL INFORMATION:
APPLICANT: No. 5981502eborn, Mathews H.M.

APPLICANT: Koch, Guus
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
TITLE OF INVENTION: APOPTOSIS IN TUMOR CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSER: Rae-Venter Law Group, P.C.
STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,001B
FILING DATE: 07-JUNE-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOVEMBER-1995

APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-JULY-1994

APPLICATION NUMBER: US 08/030,335
FILING DATE: 8-MARCH-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 11-SEP-1991

FILING DATE: 20-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEPTEMBER-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 926-6205
TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULAR TYPE: protein
HYPOTHETICAL: NO
US-08-485-001B-7

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Best Local Similarity 98.3%; Pred. No. 2.4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 121 L 121
DB 121 L 121

RESULT 4
US-08-454-121A-7

Sequence 7, Application US/08454121A
Patent No. 6071520
GENERAL INFORMATION:
APPLICANT: No. 6071520eborn, Mathews H.M.
APPLICANT: Koch, Guss
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: And Uses Based On The Viral Proteins VP1, VP2, And VP3 Or
TITLE OF INVENTION: Sequences Of That Virus Coding Therefor
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,121A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
FILING DATE: 8-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULAR TYPE: protein
HYPOTHETICAL: NO
US-08-454-121A-7

Query Match 98.9%; Score 624; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 2.4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITITLSLGGCANAPATLRSA 60
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QY 121 L 121
DB 121 L 121

RESULT 5
US-08-482-161B-7

Sequence 7, Application US/08482161B
Patent No. 6162461
GENERAL INFORMATION:
APPLICANT: No. 6162461eborn, Mathews H.M.
APPLICANT: Koch, Guss
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: And Uses Based On The Viral Proteins VP1, VP2, And VP3 Or
TITLE OF INVENTION: Sequences Of That Virus Coding Therefor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,161B
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOVEMBER-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/NL 94/00168
FILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
FILING DATE: 08-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEPTEMBER-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 926-6205
TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-482-161B-7

Query Match 98.9%; Score 624; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 2,4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLSLCCGANNAPATLRS 60

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DB 61 TADNSESTGFKNVPLRTDQPKPPSKKSCDPSEYVSELKESLITTPASRPTARRR 120

QY 121 L 121
DB 121 L 121

RESULT 6
US-09-057-963A-6
Sequence 6, Application US/09057963A
Patent No. 6217870
GENERAL INFORMATION:
APPLICANT: No. 6217870eborn, M.H.M
TITLE OF INVENTION: Chicken Anemia Virus mutants and
TITLE OF INVENTION: vaccines and uses based on the viral proteins VP1, VP2 and
TITLE OF INVENTION: VP3 or sequences of that virus coding therefor.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: RAE-VENTER LAW GROUP, P.C.
STREET: P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,963A
FILING DATE: 09-APR-1998

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,666
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 94/00168
FILING DATE: 19-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL 91/00165
FILING DATE: 11-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.04US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-057-963A-6

Query Match 98.9%; Score 624; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 2,4e-65;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLSLCCGANNAPATLRS 60
DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIGITITLSLCCGANNAPATLRS 60

QY 61 TADNSESTGFKNVPLRTDQPKPPSKKSCDPSEYVSELKESLITTPASRPTARRR 120
DB 61 TADNSESTGFKNVPLRTDQPKPPSKKSCDPSEYVSELKESLITTPASRPTARRR 120

QY 121 L 121
DB 121 L 121

RESULT 7
US-09-645-415A-58
Sequence 58, Application US/09645415A
Patent No. 6962696
GENERAL INFORMATION:
APPLICANT: Bermudez, G.
APPLICANT: King, I.
APPLICANT: Clairmont, C.
APPLICANT: Lin, S.
APPLICANT: Belcourt, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REFERENCE: 8002-059
CURRENT APPLICATION NUMBER: US/09/645,415A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/157,581

PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 60/157,637
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 58
LENGTH: 134
TYPE: PR1
ORGANISM: Bacteriophage
US-09-645-415A-58

Query Match 97.6%; Score 616; DB 2; Length 134;
Best Local Similarity 97.5%; Pred. No. 2.4e-64;
Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVPRPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60
DB 14 MNALQEDTPPGSTVPRPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 73
QY 61 TADNSETGFKNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPSRTARRR 120
DB 74 TADNSETGFKNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPSRTARRR 133
QY 121 L 121
DB 134 L 134

RESULT 8

US-09-645-415A-60
Sequence 60, Application US/09645415A
Patent No. 6962696
GENERAL INFORMATION:
APPLICANT: Bermudes, G.
APPLICANT: King, I.
APPLICANT: Claitmont, C.
APPLICANT: Lin, S.
APPLICANT: Belcourt, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
FILE REFERENCE: 8002-059
CURRENT APPLICATION NUMBER: US/09/645,415A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/157,581
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 60/157,637
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 140
TYPE: PR1
ORGANISM: Bacteriophage
US-09-645-415A-60

Query Match 97.6%; Score 616; DB 2; Length 140;
Best Local Similarity 97.5%; Pred. No. 2.6e-64;
Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVPRPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60
DB 20 MNALQEDTPPGSTVPRPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 79
QY 61 TADNSETGFKNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPSRTARRR 120
DB 80 TADNSETGFKNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPSRTARRR 139
QY 121 L 121
DB 140 L 140

RESULT 9

US-09-252-991A-25918
Sequence 25918, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25918
LENGTH: 757
TYPE: PR1
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25918

Query Match 14.0%; Score 88.5; DB 2; Length 757;
Best Local Similarity 27.9%; Pred. No. 0.14;
Matches 36; Conservative 13; Mismatches 53; Indels 27; Gaps 4;

QY 9 PPGSTVPRPTSSRPLETP-----HCREIRIGIAGITITLSCGCANARA-- 54
DB 372 PGQAGIAAPAGSHSRADGHPQOYLVAVDHRRRLRAAAGRLSLQPGADARKG 431
QY 55 ---PTLRATADNSETGFKNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPS 111
DB 432 GRPGQSGSRRRRPPRRAPRPPRTDQGCRLRQPCRP-----RLMHGPAH 481
QY 112 PRTARRR 120
DB 482 PRRRRRRR 490

RESULT 10

US-09-252-991A-30531
Sequence 30531, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30531
LENGTH: 488
TYPE: PR1
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30531

Query Match 13.5%; Score 85; DB 2; Length 488;
Best Local Similarity 30.3%; Pred. No. 0.21;
Matches 37; Conservative 10; Mismatches 41; Indels 34; Gaps 7;

QY 9 PPGSTVPRPTSSRPLETPHCREIRIGIAGITIT-----LSLGCANARAPTLRSA 60
DB 1 PP-----PTSS-----ARRAKYVGGPGIRPSTSNRPRTSSALGATTCSPWSLPR 48
QY 61 TADNSET-----GRNVVDLRTDQPKPKSKKSCDPSSEYVSELSKSLITTAAPS 111
DB 49 SADSSDTRGRDGGDQGRRLR-DQSPSTVSTAVSCSAS---AVLRPCVTVMMP 103
QY 112 PR 113

Db 104 PR 105

RESULT 11

US-09-252-991A-25561
Sequence 25561, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25561

LENGTH: 133

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25561

Query Match 13.2%; Score 83.5; DB 2; Length 133;

Best Local Similarity 27.5%; Pred. No. 0.054;

Matches 33; Conservative 12; Mismatches 36; Indels 39; Gaps 7;

19 PTTSSRP-LETPHCHREIRIGIAGITITLSLCCGN-ARAPTLRSATADN----- 64

3 PPTSPAPITSSCR-TVGIA-----TAATSCNPTKARTTSASRVNSTDDSIIVSPT 56

65 ---SSTGFKNVPDLRTDQPKPSKRSKCDPSEYRVSEKESLITAPSRPTARRIRL 121

57 SRFMKRTARKTPTSTANPTPS-----PTPTRASR-----PRPATRRKSNV 100

RESULT 12

US-09-252-991A-24427
Sequence 24427, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24427

LENGTH: 384

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24427

Query Match 13.2%; Score 83.5; DB 2; Length 384;

Best Local Similarity 25.0%; Pred. No. 0.22;

Matches 38; Conservative 21; Mismatches 36; Indels 57; Gaps 9;

8 TTPGP-----STVFRPPTSS-----RPLETHCHREIRIGIAGITITLSLCCG 49

49 TTPWPLRKSNSSGTSASSVRSPRASSRRACSSRC-----TTSATICRC 98

50 ANARAPTLRSATADNSEST-----GFKNVPDLRTDQ-KPPSKK-----R 88

99 ASRRALLIALCALCSASTSMSPATGAGAN-----SQAPMKPPANLAPTTQAPASISNR 153

QY 89 SCDPSEYRV--SELKSLITTPAS-RPRTARR 117
Db 154 GCRWTERAAPRCRLKRMCMCTYPSYGPAVAKR 185

RESULT 13

US-09-252-991A-26926
Sequence 26926, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26926

LENGTH: 195

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26926

Query Match 13.0%; Score 82; DB 2; Length 195;

Best Local Similarity 28.0%; Pred. No. 0.13;

Matches 37; Conservative 14; Mismatches 49; Indels 32; Gaps 8;

5 QEDTPGSPVTRP-----PTSSRPLETHCHREIRIGIAGITITLSLCCG 49

77 EKNSSPSAGCTPTCSWTACGNASCTWPTSWKVRIFVCSCT---RASITWACSGS 132

50 ANARAPTLRS-ATADNSESTGFKNVPDLRTDQPKPSKRSKCD-PSEYRVSEK--ESLI 105

133 RRAANPRLNSRATRRCASSTA-----SNWPRAACTSRCTDRASMTSASIRWASCT 184

QY 106 TTAQSPRPRTARR 117
Db 185 TSAQC-PTTARR 195

RESULT 14

US-09-252-991A-29784
Sequence 29784, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29784

LENGTH: 135

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29784

Query Match 12.9%; Score 81.5; DB 2; Length 135;

Best Local Similarity 27.8%; Pred. No. 0.094;

Matches 32; Conservative 12; Mismatches 42; Indels 29; Gaps 4;

19 PTTSSRPLETHCHREIRIGIAGITITLSLCCGNARAPTLR-----SATADNSESTGFKNV 73

16 PTTSR-----CRSIVACRARSICPCWPTTRRRPTRTTSCSAGTCIGQSRRCRST 69

QY 74 PDARTDQPKRPSKRCSDPSEY-----RVSELKESLITTAAPSRRRTARRIR 120
DB 70 PRRRTPTGPTSDRSRRPTAPSPSRMPPTPRIS-----PSSTVRSKRRLR 114

RESULT 15

US-09-902-540-10602
Sequence 10602, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10602

LENGTH: 766

TYPE: PRF

ORGANISM: Myxococcus xanthus

US-09-902-540-10602

Query Match 12.8%; Score 81; DB 2; Length 766;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 37; Conservative 19; Mismatches 57; Indels 26; Gaps 5;

QY 3 ALQED-----TPGPSTVFRP-----PTSSRPLETPHCREIRIGIAGITITLSLQCA 50
DB 340 ALQEDSADSAPTSQMPAPRARPAPSPHSSAPKPVQRRPAPGCVALRGPSVAGNGSA 399
QY 51 NARAPTLRSATADNSEST-----GKNVDPDLRTDQPK-----PSKKRSGCDPSEYRVSEL 100
DB 400 PKPAPQRRRTSEASPVSRTPRGQDSAPAAARTPRPTARQEVFAESESID---EPSDL 455
QY 101 KESLITTAAPSRRRTARRIR 119
DB 456 QTORFRSRPQRRPGADGARV 474

Search completed: April 20, 2006, 12:18:41
Job time : 48 secs

GenCore version 5.1.7
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QM protein - protein search, using sw model

Run on: April 20, 2006, 12:28:39 ; Search time 166 Seconds
(without alignments)
304,562 Million cell updates/sec

Title: US-10-083-849C-12

Perfect score: 631

Sequence: 1 MNALEDTPPGPSTVFRPPT.....ESLITTPSRPTARRRRL 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	121	4	US-10-083-849B-12 Sequence 12, Appl
2	627	99.4	121	4	US-10-083-849B-1 Sequence 1, Appl
3	626	99.2	121	4	US-10-083-849B-16 Sequence 16, Appl
4	626	99.2	121	4	US-10-083-849B-18 Sequence 18, Appl
5	626	99.2	121	4	US-10-083-849B-19 Sequence 19, Appl
6	624	98.9	121	3	US-09-740-676-7 Sequence 7, Appl
7	624	98.9	121	4	US-10-083-849B-2 Sequence 2, Appl
8	622	98.6	121	4	US-10-083-849B-10 Sequence 10, Appl
9	622	98.6	121	4	US-10-083-849B-11 Sequence 11, Appl
10	621	98.4	121	4	US-10-083-849B-14 Sequence 14, Appl
11	621	98.4	121	4	US-10-083-849B-15 Sequence 15, Appl
12	619	98.1	121	4	US-10-083-849B-13 Sequence 13, Appl
13	619	98.1	121	4	US-10-083-849B-17 Sequence 17, Appl
14	617	97.8	121	4	US-10-083-849B-58 Sequence 58, Appl
15	616	97.6	134	5	US-10-738-423-58 Sequence 58, Appl
16	616	97.6	140	5	US-10-738-423-60 Sequence 60, Appl
17	616	97.6	523	3	US-10-113-790-1 Sequence 1, Appl
18	611	96.8	133	3	US-09-949-780-4 Sequence 4, Appl
19	611	96.8	133	3	US-09-949-780-6 Sequence 6, Appl
20	611	96.8	511	3	US-09-949-780-2 Sequence 2, Appl
21	610	96.7	121	4	US-10-083-849B-7 Sequence 7, Appl
22	603	95.6	121	4	US-10-083-849B-5 Sequence 5, Appl
23	602	95.4	121	4	US-10-083-849B-6 Sequence 6, Appl
24	602	95.4	121	4	US-10-083-849B-8 Sequence 8, Appl
25	599	94.9	121	4	US-10-083-849B-9 Sequence 9, Appl
26	597	94.6	121	4	US-10-083-849B-3 Sequence 3, Appl
27	593	94.0	121	4	US-10-083-849B-4 Sequence 4, Appl

28	98	15.5	223	4	US-10-437-963-190571	Sequence 190571,
29	93.5	14.8	166	4	US-10-437-963-163025	Sequence 163025,
30	90	14.3	206	4	US-10-437-963-180157	Sequence 180157,
31	87	13.8	335	4	US-10-437-963-157638	Sequence 157638,
32	86.5	13.7	625	4	US-10-437-963-155015	Sequence 155015,
33	86	13.6	168	4	US-10-437-963-150263	Sequence 150263,
34	85	13.5	209	4	US-10-437-963-108424	Sequence 108424,
35	84	13.3	315	4	US-10-425-114-66407	Sequence 66407, A
36	84	13.3	329	4	US-10-425-115-240302	Sequence 240302,
37	83	13.2	195	4	US-10-437-963-123418	Sequence 123418,
38	83	13.2	377	4	US-10-149-818-7	Sequence 7, Appl
39	83	13.2	377	4	US-10-312-352-30	Sequence 30, Appl
40	82	13.0	159	5	US-10-732-923-5639	Sequence 5639, Ap
41	82	13.0	326	4	US-10-425-114-50335	Sequence 50335, A
42	81.5	12.9	203	4	US-10-425-115-232583	Sequence 232583,
43	81.5	12.9	216	4	US-10-767-701-57343	Sequence 57343, A
44	81.5	12.9	268	4	US-10-437-963-149247	Sequence 149247,
45	81.5	12.9	5317	4	US-10-668-767-59	Sequence 59, Appl

ALIGNMENTS

```

RESULT 1
US-10-083-849B-12
; Sequence 12, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
; APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083.849B
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.1
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Chicken anemia virus
; FEATURE:
; NAME/KEY: MOTAGEN
; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T108A of Apoptin
US-10-083-849B-12
Query Match 100.0%; Score 631; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5e-55;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNALEDTPPGPSTVFRPPTSRPLETHPCREIRIGIGITITTLSCCANARATLRS 60
DB 1 MNALEDTPPGPSTVFRPPTSRPLETHPCREIRIGIGITITTLSCCANARATLRS 60
QY 61 TADNSESFGKVPDLRTDQPKPKKSCDPSSEYRVELKESLITTPAPSRPTARRR 120
DB 61 TADNSESFGKVPDLRTDQPKPKKSCDPSSEYRVELKESLITTPAPSRPTARRR 120
QY 121 L 121
DB 121 L 121
RESULT 2
US-10-083-849B-1
; Sequence 1, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu

```

APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(121)
OTHER INFORMATION: Apoptin (a small protein derived from chicken anemia virus) encoded by PCMV-Vp3 and by GFP-Apoptin constructs
US-10-083-849B-1

Query Match 99.4%; Score 627; DB 4; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.6e-54;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60

DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60

QY 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120

DB 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120

QY 121 L 121

DB 121 L 121

RESULT 3
US-10-083-849B-16
Sequence 16, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant T108B of Apoptin
US-10-083-849B-16

Query Match 99.2%; Score 626; DB 4; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.6e-54;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60
DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60

QY 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120
DB 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 4
US-10-083-849B-18
Sequence 18, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: double point mutant T107A108A of Apoptin
US-10-083-849B-18

Query Match 99.2%; Score 626; DB 4; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.6e-54;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60

DB 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLSCGCANARAPTLRSA 60

QY 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120

DB 61 TADNSESTGFKVNPDLRTDQPKPSPKSCDSEYRVSELSKSLITTAAPSRTARRR 120

QY 121 L 121

DB 121 L 121

RESULT 5
US-10-083-849B-19
Sequence 19, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 121

TYPE: PR1
ORGANISM: Chicken anemia virus
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
OTHER INFORMATION: double point mutant T106A108A of Apoptin
US-10-083-849B-19

Query Match 99.2%; Score 626; DB 4; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.6e-54;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Db 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Qy 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Db 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Qy 121 L 121
Db 121 L 121

RESULT 6

US-09-740-676-7

Sequence 7, Application US/09740676

Publication No. US20050100552A1

GENERAL INFORMATION:

APPLICANT: Noteborn, Matheus H.M.

Koch, Guus

TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines

And Uses Based On The Viral Proteins VP1, VP2, And VP3 Or

Sequences Of That Virus Coding Therefor

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rae-Venter Law Group, P.C.

STREET: P.O. Box 60039

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/740,676

FILING DATE: 18-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/454,121

FILING DATE: 30-NOVEMBER-1995

APPLICATION NUMBER: PCT/NL 94/00168

FILING DATE: 19-JULY-1994

APPLICATION NUMBER: US 08/030,335

FILING DATE: 08-MARCH-1993

APPLICATION NUMBER: NL 9301272

FILING DATE: 20-JULY-1993

APPLICATION NUMBER: PCT/NL 91/00165

FILING DATE: 11-SEPTEMBER-1991

APPLICATION NUMBER: NL 9002008

FILING DATE: 12-SEPTEMBER-1990

ATTORNEY/AGENT INFORMATION:

NAME: Rae-Venter, Barbara

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: LEBV.003.01US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 926-6205

TELEFAX: (650) 424-8760

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-740-676-7

Query Match 98.9%; Score 624; DB 3; Length 121;
Best Local Similarity 98.3%; Pred. No. 2.5e-54;

Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Db 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Qy 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Db 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Qy 121 L 121
Db 121 L 121

RESULT 7

US-10-083-849B-2

Sequence 2, Application US/10083849B

Publication No. US20030199009A1

GENERAL INFORMATION:

APPLICANT: No. US20030199009A1eborn, Matheus

APPLICANT: Rohn, Jennifer Leigh

APPLICANT: Mumberg, Dominik

APPLICANT: Donner, Peter

TITLE OF INVENTION: Modifications of Apoptin

FILE REFERENCE: 2906-4996.1

CURRENT APPLICATION NUMBER: US/10/083,849B

PRIOR APPLICATION NUMBER: 2001-10-19

PRIOR FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 121

TYPE: PR1

ORGANISM: Chicken anemia virus

FEATURE:

NAME/KEY: MUTAGEN

LOCATION: (1)..(121)

OTHER INFORMATION: Apoptin protein encoded by pIRESneo alanine mutants

FEATURE:

NAME/KEY: MISC FEATURE

OTHER INFORMATION: Differs from Apoptin protein encoded by pcMV-vp3 and by GFP-Apop

OTHER INFORMATION: in constructs by replacement of the arginine residue at position

OTHER INFORMATION: 116 with a lysine residue

US-10-083-849B-2

Query Match 98.9%; Score 624; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 2.5e-54;

Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Db 1 MNALEDTPPGSTVFRPPTSSRPLETPHCRIRIGIAGITTTSLCCGANARAPTLRSA 60
Qy 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Db 61 TADNSETGFKNVPLDRTDQPKPSKRSQPSSEYRVSELKESLITTAAPSRTARRRIR 120
Qy 121 L 121
Db 121 L 121

```
RESULT 8
US-10-083-849B-10
; Sequence 10, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
; APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 121
; TYPE: PRF
; ORGANISM: Chicken anemia virus
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T106A of Apoptin
US-10-083-849B-10

Query Match      98.6%; Score 622; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 3.9e-54;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
DB 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
QY 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
DB 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 9
US-10-083-849B-11
; Sequence 11, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
; APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRF
; ORGANISM: Chicken anemia virus
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T107A of Apoptin
US-10-083-849B-11
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Query Match      98.6%; Score 622; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 3.9e-54;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
DB 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
QY 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
DB 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 10
US-10-083-849B-14
; Sequence 14, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
; APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 121
; TYPE: PRF
; ORGANISM: Chicken anemia virus
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T106E of Apoptin
US-10-083-849B-14

Query Match      98.4%; Score 621; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 4.9e-54;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
DB 1 MMALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSLCCGANNAPFLRSA 60
QY 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
DB 61 TADNSESTGFKVNPDLRTDQPKPSKRSQDSEYVSELKESLITTAAPSRTARRR 120
QY 121 L 121
DB 121 L 121

RESULT 11
US-10-083-849B-15
; Sequence 15, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
; APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
```

;; CURRENT FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/242,397
;; PRIOR FILING DATE: 2000-10-20
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 15
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Chicken anemia virus
;; FEATURE:
;; NAME/KEY: MUTAGEN
;; LOCATION: (1)..(121)
;; OTHER INFORMATION: single point mutant T107E of Apoptin
US-10-083-849B-15

Query Match 98.4%; Score 621; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 4, 3e-54;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 60
Db 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 60
Qy 61 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 120
Db 61 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 120
Qy 121 L 121
Db 121 L 121

RESULT 12
US-10-083-849B-13
;; Sequence 13, Application US/10083849B
;; Publication No. US20030199009A1
;; GENERAL INFORMATION:
;; APPLICANT: Rohn, Jennifer Leigh
;; APPLICANT: Mumberg, Dominik
;; APPLICANT: Donner, Peter
;; TITLE OF INVENTION: Modifications of Apoptin
;; FILE REFERENCE: 2906-4996.1
;; CURRENT APPLICATION NUMBER: US/10/083,849B
;; CURRENT FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/242,397
;; PRIOR FILING DATE: 2000-10-20
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 13
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Chicken anemia virus
;; FEATURE:
;; NAME/KEY: MUTAGEN
;; LOCATION: (1)..(121)
;; OTHER INFORMATION: single point mutant P109A of Apoptin
US-10-083-849B-13

Query Match 98.1%; Score 619; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 7, 8e-54;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 60
Db 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 60
Qy 61 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 120
Db 61 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 120
Qy 121 L 121
Db 121 L 121

Db 121 L 121

RESULT 13
US-10-488-363-2
;; Sequence 2, Application US/10488363
;; Publication No. US20050169939A1
;; GENERAL INFORMATION:
;; APPLICANT: Leonard, Joan
;; APPLICANT: Rosenberger, John
;; APPLICANT: Cowen, Barrett
;; TITLE OF INVENTION: CHICKEN ANEMIA VIRUS VACCINE FROM CELL
;; FILE REFERENCE: 02108, 0003U3
;; CURRENT APPLICATION NUMBER: US/10/488,363
;; CURRENT FILING DATE: 2004-03-02
;; PRIOR APPLICATION NUMBER: PCT/US02/28551
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: 60/317,239
;; PRIOR FILING DATE: 2001-09-05
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 786
;; TYPE: PRT
;; ORGANISM: Chicken anemia virus
US-10-488-363-2

Query Match 98.1%; Score 619; DB 5; Length 786;
Best Local Similarity 98.3%; Pred. No. 7, 2e-53;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 60
Db 666 MNALQEDTPPGSTVFRPPTSSRPLETPHCRIRIGIGITITLTLSCGANNAPAPTLRSA 725
Qy 61 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 120
Db 726 TADNSESTGFKNVPLRTDQPKPSKRSQDPSSEYRVSELKSLITTTAPSRPTARRRIR 785
Qy 121 L 121
Db 786 L 786

RESULT 14
US-10-083-849B-17
;; Sequence 17, Application US/10083849B
;; Publication No. US20030199009A1
;; GENERAL INFORMATION:
;; APPLICANT: Rohn, Jennifer Leigh
;; APPLICANT: Mumberg, Dominik
;; APPLICANT: Donner, Peter
;; TITLE OF INVENTION: Modifications of Apoptin
;; FILE REFERENCE: 2906-4996.1
;; CURRENT APPLICATION NUMBER: US/10/083,849B
;; CURRENT FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/242,397
;; PRIOR FILING DATE: 2000-10-20
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 17
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Chicken anemia virus
;; FEATURE:
;; NAME/KEY: MUTAGEN
;; LOCATION: (1)..(121)
;; OTHER INFORMATION: double point mutation T106A107A of Apoptin
US-10-083-849B-17

Query Match 97.8%; Score 617; DB 4; Length 121;

Best Local Similarity 97.5%; Pred. No. 1.2e-53;
Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSICGCANARAPTLRSA 60
Db 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSICGCANARAPTLRSA 60

QY 61 TADNSESTGFKVVPDLRTDQPKPSKRSQDPSEYRVSELSKSLTTAPSRPRTARRR 120
Db 61 TADNSESTGFKVVPDLRTDQPKPSKRSQDPSEYRVSELSKSLTAATPSRPTARRR 120

QY 121 L 121
Db 121 L 121

RESULT 15

US-10-738-423-58
; Sequence 58, Application US/10738423
; Publication No. US20040229338A1
; GENERAL INFORMATION:
; APPLICANT: Bermudez, G.
; APPLICANT: King, I.
; APPLICANT: Claitmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/10/738,423
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Bacteriophage
US-10-738-423-58

Query Match 97.6%; Score 616; DB 5; Length 134;

Best Local Similarity 97.5%; Pred. No. 1.8e-53;
Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSICGCANARAPTLRSA 60
Db 14 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITTTLSICGCANARAPTLRSA 73

QY 61 TADNSESTGFKVVPDLRTDQPKPSKRSQDPSEYRVSELSKSLTTAPSRPRTARRR 120
Db 74 TADNSESTGFKVVPDLRTDQPKPSKRSQDPSEYRVSELSKSLTTAPSRPTARRR 133

QY 121 L 121
Db 134 L 134

Search completed: April 20, 2006, 12:32:20
Job time : 167 secs

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QM protein - protein search, using sw model

Run on: April 20, 2006, 12:29:44 ; Search time 27 Seconds
(without alignments)
197.198 Million cell updates/sec

Title: US-10-083-849c-12

Perfect score: 631
Sequence: 1 MNAQEDTPPGSTVFRRPPT.....ESLITTAPEPRTRARRIRL 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
1: /SIDS/prodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /SIDS/prodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /SIDS/prodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /SIDS/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
5: /SIDS/prodata/2/pubppaa/US09_NEW_PUB.pep:*
6: /SIDS/prodata/2/pubppaa/US10_NEW_PUB.pep:*
7: /SIDS/prodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /SIDS/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	98.9	121	US-11-204-980-1	Sequence 1, Appli
2	616	97.6	134	US-11-082-544-58	Sequence 58, Appli
3	616	97.6	140	US-11-082-544-60	Sequence 60, Appli
4	404	64.0	80	US-11-204-980-16	Sequence 16, Appli
5	196	31.1	40	US-11-204-980-17	Sequence 17, Appli
6	86.5	13.7	183	US-11-096-568A-17740	Sequence 17740, A
7	86	13.6	319	US-11-096-568A-24347	Sequence 24347, A
8	78	12.4	300	US-11-096-568A-27037	Sequence 27037, A
9	77	12.2	493	US-11-096-568A-11657	Sequence 11657, A
10	76	12.0	319	US-11-096-568A-24535	Sequence 24535, A
11	75	11.9	238	US-11-096-568A-15924	Sequence 15924, A
12	75	11.9	267	US-11-096-568A-1120	Sequence 1120, Ap
13	74	11.7	491	US-11-069-642-137	Sequence 137, App
14	74	11.7	554	US-11-096-568A-17691	Sequence 17691, A
15	73.5	11.6	164	US-11-096-568A-26546	Sequence 26546, A
16	73.5	11.6	181	US-11-096-568A-26261	Sequence 26261, A
17	73.5	11.6	197	US-11-096-568A-26545	Sequence 26545, A
18	72.5	11.5	665	US-11-124-368A-289	Sequence 289, App
19	72.5	11.5	899	US-11-124-368A-290	Sequence 290, App
20	72.5	11.5	1439	US-11-124-368A-291	Sequence 291, App
21	72	11.4	224	US-11-096-568A-1294	Sequence 1294, A
22	71.5	11.3	210	US-11-096-568A-18268	Sequence 18268, A
23	71.5	11.3	251	US-11-096-568A-18174	Sequence 18174, A
24	71.5	11.3	406	US-11-096-568A-12552	Sequence 12552, A
25	70.5	11.2	312	US-11-096-568A-9235	Sequence 9235, Ap

26	70.5	11.2	954	US-11-188-298-16512	Sequence 16512, A
27	70	11.1	198	US-11-096-568A-9882	Sequence 9882, Ap
28	69.5	11.0	189	US-11-096-568A-13837	Sequence 13837, A
29	69.5	11.0	211	US-11-124-368A-187	Sequence 187, App
30	69.5	11.0	30	US-11-096-568A-22109	Sequence 22109, A
31	69.5	11.0	312	US-11-096-568A-12515	Sequence 12515, A
32	69.5	11.0	1474	US-11-188-298-6321	Sequence 6321, Ap
33	69	10.9	278	US-11-096-568A-25421	Sequence 25421, A
34	69	10.9	286	US-11-096-568A-25420	Sequence 25420, A
35	69	10.9	287	US-11-072-512-2485	Sequence 2485, Ap
36	69	10.9	293	US-11-096-568A-12504	Sequence 12504, A
37	69	10.9	315	US-11-096-568A-25419	Sequence 25419, A
38	69	10.9	382	US-11-096-568A-26984	Sequence 26984, A
39	69	10.9	456	US-11-190-339-2	Sequence 2, Appli
40	69	10.9	839	US-10-242-586-54	Sequence 54, Appl
41	69	10.9	839	US-10-242-902-54	Sequence 54, Appl
42	69	10.9	839	US-10-243-116-54	Sequence 54, Appl
43	69	10.9	839	US-10-243-136-54	Sequence 54, Appl
44	69	10.9	839	US-10-243-189-54	Sequence 54, Appl
45	69	10.9	839	US-10-243-215-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-11-204-980-1
Sequence 1, Application US/11204980
Publication No. US20060057652A1
GENERAL INFORMATION:
APPLICANT: Green, Michael
APPLICANT: Hellman, Deatin
TITLE OF INVENTION: METHODS FOR IDENTIFYING THERAPEUTIC
FILE REFERENCE: 07917-196001
CURRENT APPLICATION NUMBER: US/11/204,980
CURRENT FILING DATE: 2005-08-15
PRIOR APPLICATION NUMBER: US 60/601,494
PRIOR FILING DATE: 2004-08-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 121
TYPE: PRT
ORGANISM: Chicken anemia virus
US-11-204-980-1

Query Match 98.9%; Score 624; DB 7; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.9e-57;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNAQEDTPPGSTVFRRPPTSSRPLETHPCREIRIGITITSLCCANARAPTLSA 60
DB 1 MNAQEDTPPGSTVFRRPPTSSRPLETHPCREIRIGITITSLCCANARAPTLSA 60
QY 61 TADNSETGFNVVDLTDOPEKPSKRSKSCDPSERYSELKESLITTPAPSPRTARRIR 120
DB 61 TADNSETGFNVVDLTDOPEKPSKRSKSCDPSERYSELKESLITTPAPSPRTARRIR 120
QY 121 L 121
DB 121 L 121
RESULT 2
US-11-082-544-58
Sequence 58, Application US/11082544
Publication No. US20050249706A1
GENERAL INFORMATION:
APPLICANT: Bernudes, G.
APPLICANT: King, I.
APPLICANT: Clairmont, C.

APPLICANT: Lin, S.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 FILE REFERENCE: 8002-059
 CURRENT APPLICATION NUMBER: US/11/082,544
 PRIOR FILING DATE: 2005-03-17
 PRIOR APPLICATION NUMBER: US/09/645,415
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: 60/157,581
 PRIOR FILING DATE: 1999-10-04
 PRIOR APPLICATION NUMBER: 60/157,637
 PRIOR FILING DATE: 1999-10-04
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 58
 LENGTH: 134
 TYPE: PRT
 ORGANISM: Bacteriophage
 US-11-082-544-58

Query Match 97.6%; Score 616; DB 7; Length 134;
 Best Local Similarity 97.5%; Pred. No. 1,4e-56;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLISCGCANRAPTLRSA 60
 DB 14 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLISCGCANRAPTLRSA 73
 QY 61 TADNSESTGFKNVVDLRTDQPKPSKRCSDPEYRVSELSLITTPSRPTARRR 120
 DB 74 TADNSENTGFKNVVDLRTDQPKPSKRCSDPEYRVSELSLITTPSRPTARRR 133
 QY 121 L 121
 DB 134 L 134

RESULT 3
 US-11-082-544-60
 Sequence 60, Application US/11082544
 Publication No. US20050249706A1
 GENERAL INFORMATION:
 APPLICANT: Bermudes, G.
 APPLICANT: King, I.
 APPLICANT: Clairmont, C.
 APPLICANT: Lin, S.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 FILE REFERENCE: 8002-059
 CURRENT APPLICATION NUMBER: US/11/082,544
 CURRENT FILING DATE: 2005-03-17
 PRIOR APPLICATION NUMBER: US/09/645,415
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: 60/157,581
 PRIOR FILING DATE: 1999-10-04
 PRIOR APPLICATION NUMBER: 60/157,637
 PRIOR FILING DATE: 1999-10-04
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 60
 LENGTH: 140
 TYPE: PRT
 ORGANISM: Bacteriophage
 US-11-082-544-60

Query Match 97.6%; Score 616; DB 7; Length 140;
 Best Local Similarity 97.5%; Pred. No. 1.5e-56;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLISCGCANRAPTLRSA 60

DB 20 MNALQEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAGITITLISCGCANRAPTLRSA 79
 QY 61 TADNSESTGFKNVVDLRTDQPKPSKRCSDPEYRVSELSLITTPSRPTARRR 120
 DB 80 TADNSENTGFKNVVDLRTDQPKPSKRCSDPEYRVSELSLITTPSRPTARRR 139
 QY 121 L 121
 DB 140 L 140

RESULT 4
 US-11-204-980-16
 Sequence 16, Application US/11204980
 Publication No. US20060057652A1
 GENERAL INFORMATION:
 APPLICANT: Green, Michael
 APPLICANT: Hellman, Joseph
 APPLICANT: Teodoro, Jose G.
 TITLE OF INVENTION: METHODS FOR IDENTIFYING THERAPEUTIC
 AGENTS AND FOR TREATING DISEASE
 FILE REFERENCE: 07917-196001
 CURRENT APPLICATION NUMBER: US/11/204,980
 CURRENT FILING DATE: 2005-08-15
 PRIOR APPLICATION NUMBER: US 60/601,494
 PRIOR FILING DATE: 2004-08-13
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 16
 LENGTH: 80
 TYPE: PRT
 ORGANISM: Chicken anemia virus
 US-11-204-980-16

Query Match 64.0%; Score 404; DB 7; Length 80;
 Best Local Similarity 97.5%; Pred. No. 6e-35;
 Matches 78; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 42 TITLISCGCANRAPTLRSATADNSESTGFKNVVDLRTDQPKPSKRCSDPEYRVSELS 101
 DB 1 TITLISCGCANRAPTLRSATADNSESTGFKNVVDLRTDQPKPSKRCSDPEYRVSELS 60
 QY 102 ESLITTPSRPTARRRRL 121
 DB 61 ESLITTPSRPTARRRRL 80

RESULT 5
 US-11-204-980-17
 Sequence 17, Application US/11204980
 Publication No. US20060057652A1
 GENERAL INFORMATION:
 APPLICANT: Green, Michael
 APPLICANT: Hellman, Joseph
 APPLICANT: Teodoro, Jose G.
 TITLE OF INVENTION: METHODS FOR IDENTIFYING THERAPEUTIC
 AGENTS AND FOR TREATING DISEASE
 FILE REFERENCE: 07917-196001
 CURRENT APPLICATION NUMBER: US/11/204,980
 CURRENT FILING DATE: 2005-08-15
 PRIOR APPLICATION NUMBER: US 60/601,494
 PRIOR FILING DATE: 2004-08-13
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 17
 LENGTH: 40
 TYPE: PRT
 ORGANISM: Chicken anemia virus
 US-11-204-980-17

Query Match 31.1%; Score 196; DB 7; Length 40;
 Best Local Similarity 95.0%; Pred. No. 7.7e-14;
 Matches 38; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 82 KPSPKRSQDSEYRVSELSKESLITTAAPSRRARRRL 121
Db 1 KPSPKRSQDSEYRVSELSKESLITTPSRPRTAKRIRL 40

RESULT 6
US-11-096-568A-17740

Sequence 17740, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 17740
LENGTH: 183
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(183)
OTHER INFORMATION: Ceres Seq. ID no. 12360044
US-11-096-568A-17740

Query Match 13.7%; Score 86.5; DB 7; Length 183;
Best Local Similarity 26.5%; Pred. No. 0.092; Indels 43; Gaps 5;

Matches 31; Conservative 9; Mismatches 34; Indels 43; Gaps 5;

QY 8 TPSPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCANARAP-----TUSATAD 63
Db 30 SPPTPP--QPSPFPGPPSPAPARRR-----CSCGAAPSPAPYTPSRRT 75
QY 64 NSESTGFKNVVDLTDQPKPSKRSQDSEYRVSELSKESLITTAAPSRRARRR 120
Db 76 PASSR-----PPRRPRRRRSCP-----RTTPSRPRLPRLARR 107

RESULT 7
US-11-096-568A-24347

Sequence 24347, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 24347
LENGTH: 319
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(319)
OTHER INFORMATION: Ceres Seq. ID no. 12434866
US-11-096-568A-24347

Query Match 13.6%; Score 86; DB 7; Length 319;
Best Local Similarity 26.1%; Pred. No. 0.2; Indels 30; Gaps 4;

Matches 30; Conservative 14; Mismatches 41; Indels 30; Gaps 4;

QY 10 PGSPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCANARAPTLRSATAD 63
Db 191 PSPSPTRPSPTR-----CRSSTTARASASARLCSRSSSTMAASSRSTSSAATSL 244
QY 64 NSESTGFKNVVDLTDQPKPSKRSQDSEYRVSELSKESLITTAAPSRRARRR 118

Db 245 ASSAVAFPCPPTMTHRRPDS-----PS-----PRSPTPSLARRR 281

RESULT 8
US-11-096-568A-27037

Sequence 27037, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27037
LENGTH: 300
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(300)
OTHER INFORMATION: Ceres Seq. ID no. 1366262
US-11-096-568A-27037

Query Match 12.4%; Score 78; DB 7; Length 300;
Best Local Similarity 25.2%; Pred. No. 1.2; Indels 30; Gaps 4;

Matches 29; Conservative 14; Mismatches 42; Indels 30; Gaps 4;

QY 10 PGSPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCANARAPTLRSATAD 63
Db 172 PSPSPTRPSPTR-----CRSSTTARASASARLCSRSSSTMAASSRSTSSAATSL 225
QY 64 NSESTGFKNVVDLTDQPKPSKRSQDSEYRVSELSKESLITTAAPSRRARRR 118
Db 226 ASSAVACPTCPPTMTHRRPDS-----PS-----PRSPTPSLARRR 282

RESULT 9
US-11-096-568A-11657

Sequence 11657, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 11657
LENGTH: 493
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(493)
OTHER INFORMATION: Ceres Seq. ID no. 15219800
US-11-096-568A-11657

Query Match 12.2%; Score 77; DB 7; Length 493;
Best Local Similarity 27.1%; Pred. No. 2.8; Indels 42; Gaps 6;

Matches 39; Conservative 8; Mismatches 55; Indels 42; Gaps 6;

QY 8 TPSPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCCANARAPTLRSATAD 59
Db 128 SPSPPT--RPSASTPSRPPTR--ASGPG---ASTGSPSPSATRRSRPSAARPR 179
QY 60 -----ATADNSESTGFKNVVDLTDQPKPSKRSQD-----S 93
Db 180 RSAPASATRTTAPTTTASATSRTRPPSPRTSSPTGSSSSRSPPTSPSPSPPTS 239
QY 94 EYRVSELSKESLITTAAPSRRARRR 117

Db 240 PRTCSAAPTSTTAPTASTPRK 263

RESULT 10
US-11-096-568A-24535

Sequence 24535, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 24535
LENGTH: 319
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(319)
OTHER INFORMATION: Ceres Seq. ID no. 12435624
US-11-096-568A-24535

Query Match 12.0%; Score 76; DB 7; Length 319;
Best Local Similarity 29.3%; Pred. No. 2.2;
Matches 34; Conservative 10; Mismatches 46; Indels 26; Gaps 6;

QY 9 PPGSTVFRPPPTSSRPLETHCHREIRIGITITSLGCGANARAPTIRSATDMS--- 65
PSPSPS---PSPHPR-APTSPSASLGTIRSAT-----APASPPSPRSAPASAPRP 154

Db 109
QY 66 -ESTFKNVDPD---TDQPKPPSKKSCDPSSEYRVELKESLITAPSRPTAR 117
DB 155 CPSTPRACRSARSGAPPRPPPPRPTSPSSAR-----SAATTSSRSGSSRRR 205

RESULT 11

US-11-096-568A-15924
Sequence 15924, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 15924
LENGTH: 238
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(238)
OTHER INFORMATION: Ceres Seq. ID no. 12349596
US-11-096-568A-15924

Query Match 11.9%; Score 75; DB 7; Length 238;
Best Local Similarity 27.2%; Pred. No. 1.9;
Matches 34; Conservative 12; Mismatches 65; Indels 14; Gaps 4;

QY 6 EDTPPGP--STVFRPPPTSSRPLETHPC-----REIRIGITITSLGCGANARAP 55
DB 76 OPTPLSPRRARAWRPPTSSPGTPTSTPTAPRWIR---SGGDPITSRRCRTSRP 132
QY 56 TIRSATADNSESITGFKNVDPDRTDQPKPPSKKSCDPSSEYRVELKESLITAPSRPTA 115
DB 133 TC-GASSSTGSGSRSPRSTSSSRTRSTSPJLMSTASSPSRSTRAVTSCTSSIALPFCSLPRSS 191

QY 116 RRRIR 120
DB 192 RRSAR 196

RESULT 12

US-11-096-568A-1120
Sequence 1120, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1120
LENGTH: 267
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(267)
OTHER INFORMATION: Ceres Seq. ID no. 13600172
US-11-096-568A-1120

Query Match 11.9%; Score 75; DB 7; Length 267;
Best Local Similarity 29.5%; Pred. No. 2.2;
Matches 38; Conservative 11; Mismatches 54; Indels 26; Gaps 5;

QY 4 LOEDTPPGSTVFRPPPT---SRPLETHCHREIRIGITITSLGCGANARAPTIR 59
DB 40 LAATTRPTGSPGPPPPARWSRRCTPFMAVLKRVVAGLITSPKTYVDATR-PMQPA 98

QY 60 ATADNSESITGFKNVDP-----LRTDQ-----KPPSKKSCDPSSEYRVELKES 103
DB 99 ATTNNSS-----LPSLRGSRRLRLDAPVVRASPLPSSSTAPLRTSCHRQSCRHS 153

QY 104 LITTAASRP 112
DB 154 LLSAARSRP 162

RESULT 13

US-11-069-642-137
Sequence 137, Application US/11069642
Publication No. US20050260626A1
GENERAL INFORMATION:
APPLICANT: LORENS, JAMES B.
APPLICANT: PRAY, TODD R.
APPLICANT: KINSELA, TODD M.
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
FILE REFERENCE: RIGL-022CIP3
CURRENT APPLICATION NUMBER: US/11/069,642
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 10/232,758
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 10/422,536
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/800,770
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/187,130
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 168
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
US-11-069-642-137

Query Match 11.7%; Score 74; DB 7; Length 491;
 Best Local Similarity 26.2%; Pred. No. 5.8;
 Matches 34; Conservative 13; Mismatches 51; Indels 32; Gaps 3;

QY 4 LOEDTPPGSTVFRPPTSSRPLETPHCREIRIGIAG-----ITITLSLGC 50
 DB 142 LOEKRPSSSHLVSRPSTSSRRRAISTENSDLSERGRKRSISLSPBSIALCV 201
 QY 51 NARAPLRSATADNSESSTGFKNVPLDR-----TDQPKPPSKRSCDPSE 94
 DB 202 IREICERS--SSSTGTPSNPDLDAGVSEHSGDWLQDQSVSDQFVFEVESLSDSD 258
 QY 95 YRVSELESL 104
 DB 259 YSLSEGOEL 268

RESULT 14

US-11-096-568A-17691
 ; Sequence 17691, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 17691
 ; LENGTH: 554
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(554)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12359830
 ; US-11-096-568A-17691

Query Match 11.7%; Score 74; DB 7; Length 554;
 Best Local Similarity 26.8%; Pred. No. 6.7;
 Matches 33; Conservative 15; Mismatches 51; Indels 24; Gaps 6;

QY 9 PPGSTVFRPPTSSRP-----LETPHCREIRIGIAGITITLSLGCANAPAPTL 57
 DB 34 PPPPA-----PPCRSRDLDLRMGTVGPGSTTPPPR--VRMAMRKENPVLTNACQASNGR--IT 86
 QY 58 RSATADNSESSTG-FKXVPLRLTDQPKPPSKRSCDPSEYRVSELESLITTPASRPRTAR 116
 DB 87 RAQAAANRRSFGAFPSVP-----LPKTERKOTAGOKARGSSYDNTSASVALSGPQPR 141
 QY 117 RRI 119
 DB 142 RTV 144

RESULT 15

US-11-096-568A-26546
 ; Sequence 26546, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 26546
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays

FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(164)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15222658
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (48)-(48)
 ; OTHER INFORMATION: Xaa is any aa, unknown or other
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (49)-(49)
 ; OTHER INFORMATION: Xaa is any aa, unknown or other
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (53)-(53)
 ; OTHER INFORMATION: Xaa is any aa, unknown or other
 ; US-11-096-568A-26546

Query Match 11.6%; Score 73.5; DB 7; Length 164;
 Best Local Similarity 29.4%; Pred. No. 1.8;
 Matches 25; Conservative 8; Mismatches 39; Indels 13; Gaps 3;

QY 13 STVFRPP--TSSRPLETPHCREIRIGIAGITITLSLC--GCANAPAPLRSATADNSES 67
 DB 67 SLMWPPGASTSRPFPAPWRRRCRPPCGWECTGRCCSSACCSGSPPT-----SPG 118
 QY 68 TGFKNVPLRLTDQPKPPSKRSCDP 92
 DB 119 TAPSPRPATSATPSSPCAVRSCPP 143

Search completed: April 20, 2006, 12:32:52
 Job time : 27 secs